STIC-Biotech/ChemLib

188683

From:

Whiteman, Brian

Sent:

Thursday, May 04, 2006 12:56 PM

To: Subject: STIC-Biotech/ChemLib FW: seg search

10659800

SEQ ID NO 6 against AA and DNA
1) issued us patents and published us patent applications
2) commercial databases

FOR DNA limit to 500 nucleotides or less.

Thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764 RE

Type of Search								
NA# AA#:								
S/L: Oligomer:								
Encode/Tran								
Structure #:_	Text:							
Inventor: Litigation:								

Vendors and cost where applicable
STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

- Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.
- Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbm (Published_Applications_NA_New).

 Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Maximum Match 100%
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Q6H12 BRARE
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COA as substrates.
CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA

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EMBL; BC015762; AAAH15762.1;
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Matches 471
                                                                                                                                                                                               TRÂNSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops (Green monkey) ((Eukaryota, Metazoa, Chordata, Craniata, Mammalia, Eutheria, Euarchontoglires, Procercopithecidae, Cercopithecidae, Cerc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 2
1 CERAE
DGAT1 CI
Q9GMF1;
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16-OCT-2001 (Rel. 40, Last sequence update)
10-NAY-2005 (Rel. 47, Last annotation updat
Diacylglycerol O-acyltransferase 1 (EC 2.3.
                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004299; MBOAT fam. Pfam; PF03062; MBOAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF236018; AAF98557.1; -; mRNA.
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Name=DGAT1; Synonyms=DGAT;
                                                                                                                                                                                                                                                                                                                                                                                                  Acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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SIMILARITY: Belongs to the membrand-bound
Sterol o-acyltransferase subfamily.
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CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    triacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Swiss-Prot entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restranglering as its content is in no way modified and this easy
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                                                    MGDR----GSSRRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAPANKDGDA
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B; Mismatches
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ca; Vertebrata;
; Primates; Cata
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RESULT 3
Q8BHI5_RAT PRELIMINARY;
AC Q8BHI5;
AC Q8BHI5;
AC Q8BHI5;
DT 01-MAR-2003 (TYENBLYE1. 23, C4
DT 01-MAR-2003 (TYENBLYE1. 29, L4
DT 01-FEB-2005 (TYENBLYE1. 29, L4
DT 01-FE
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Best Loc
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Harada Y., Watanabe T.K., Tanigami A.;

EMBL; AB062750; BAC43739.1; -; mRNA.

EMBL; AB062761; BAC43741.1; -; mRNA.

EMBL; AB062762; BAC43742.1; -; mRNA.

EMBL; AB062763; BAC43742.1; -; mRNA.

EMBL; AB062763; BAC43743.1; -; mRNA.

EMBL;
                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03062; MBOAT; 1. Acyltransferase; Transferase. SEQUENCE 500 AA; 57086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Fischer344/DuCrj, OLETF/Otk, LETO/Otk,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                            Match
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--NKDGDAGVGSGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLI
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                                                                                                                                                                                                                                      Score 2299.5; DB 2;
Pred. No. 3.6e-176;
6; Mismatches 31;
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QBSQBO BOVIN

OBSQBO BOVIN

ID OBSQBO BOVIN PRELIMINARY; PRT; 489 AA.

AC QBSQBO;

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 24, Last annotation update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DI 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE C. 2.3.1.20)

CS Bos taurus (Bovine)

CS CEUkaryota; Metazoa; Chordata; Craniata; Vertebrata; last annotation; Condate; Chordata; Cetartiodactyla;

Peccora; Bovidae; Bovinae; Bos.

OC Eukaryota; Bevidae; Bos.

OC Eukaryota; Bovidae; Bos.

OC Eukaryota; Bovidae; Bos.

OC Eukaryota; Bovidae; Bos.

OC Eukaryota; PaxID=9913;

RN NUCLEOTIDE SEQUENCE.

RP NUCLEOTIDE SEQUENCE.

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                                                                                                                                                                                                  Query Match
Best Local S
Matches 434
                                                                                                                                                                                                                                                                                                                                  "Positional candidate cloning of a QTL in dairy cattle of a missense mutation in the bovine DEAT1 gene with milk yield and composition.";
Genome Res. 12:222-231(2002).
EMBL; AY065621; AAL49962.1; -; Genomic DNA.
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0004144; F:diacyllycerol O-acyltransferase act GO; GO:0004144; F:diacyllycerol O-acyltransferase activity; IEA.
R GO; GO:0016740; F:transferase activity; IEA.
R InterPro; IPR004299; MBOAT; AR InterPro; IPR004299; MBOAT; ACYltransferase; Transferase.
SEQUENCE 489 AA; 55601 MM; 4066D8C1B6743253 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
MEDLINE=21686133; PubMed=11827942; DOI=10.1101/gr.224202;
Grisart B., Coppieters W., Farnir F., Karim L., Ford C.,
Gambisano N., Mni M., Reid S., Simon P., Spelman R., Geor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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   GVGSGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDP 117
                                                                                                                               MGDR----GSSRRRRTGSRPSSHGGGGPAAABEEEVRDAAAGPDVGAAGDAPAPAPNKDGDA
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|||||||||||||::|||||||||
ELASAFFHEYLVSIPLRMFRLMAFTAMMAQVPLAWIVNRFFQGNYGNAAVWVTLIIGQPV
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                                                                   MGDRGGAGGSRRRRTGSRPSIQGGSGPAAAEEEVR-----DVGAGGDAPVRDTDKDGDV
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                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                              88.4%;
                                                                                                                                                                                                         15;
                                                                                                                                                                                                      Score 2292.5; DB 2,
Pred. No. 1.3e-175;
5; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                            4066D8C1B6743253 CRC64;
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                                                                                                                                                                                                                                                                     NÜCLEOTIDE SEQUENCE.

MEDLINS-22103627; PubMed=12077321; DOI=10.1073/pnas.142293799;

MINTER A., Kramer W., Werner F.A.O., Kollers S., Kata S.,

A Winter A., Kramer W., Werner F.A.O., Kollers S., Kata S.,

A Durstewitz G., Buitkamp J., Womack J.E., Thaller G., Fries R.;

"Association of a lysine-232[c]s1134]alanine polymorphism in a bovine

gene encoding acyl-CoA:diacylglycerol acyltransferase (DGAT1) with

variation at a quantitative trait locus for milk fat content.";

rariation at a quantitative trait locus for milk fat content.";

Proc. Natl. Acad. Sci. U.S.A. 99:9305(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:9305(2002).

EMBL; AJ318490; CAC866391.1; -; Genomic_DNA.

RR GO; GO:0008415; F.acyltransferase activity; IEA.

RGO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                            Query Match
Best Local S
Matches 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBMK44 BOVIN PRELIMINARY; PRT; 489 AA.

OBMK44;
OBMK44;
O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Acyl-CoA:1,3-diacylglycerol O-transferase (EC 2.3.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                   Acyltransferase; Tr
SEQUENCE 489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLIQQWMVPAIQNSMKPFKDMDYSRIVERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELM
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                                                                                                   MGDR---GSSRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAPNKDGDA
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                                                        MGDRGGAGGSRRRRTGSRPSIQGGSGPAAAEEEVR-----DVGAGGDAPVRDTDKDGDV
                                                                                                                                               Conservative
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A; 55445 MW;
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C STRAIN-CS7BL/6J; TISSUE=Tongue;

K MEDLINE=22354683; PubMed=12466851; DOI*10.1038/nature01266;

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RA Schriml L.M., Kanapin A., Brusic V., Chothia C., Corbani L.E., Cousins S.

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.

RA Gasseerland T.A., Pletcher C.F., Forrest A., Frazer K.S.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
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                                                                                                                                                                                                                                                                                                                                                                  "Identification of a gene encoding an acyl CoA:diacylglycerol acyltransferase, a key enzyme in triacylglycerol synthesis.", Proc. Natl. Acad. Sci. U.S.A. 95:13018-13023(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cases S., Smith S.J.,
Novak S., Collins C.,
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MEDLINE=99007259;
                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9789033; DOI=10.1073/pnas.95.3.
J., Zheng Y.-W., Myers H.M., Lear S.F.
C., Welch C.B., Lusid A.J., Erickson
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RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A.; Schneider C., Semple C.A., Setou M., Shimada K., RA Sultana R., Takenaka Y., Taylor M.S., Teaddale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., RA Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S., RA RA Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S., RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., RA Wiyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full:length cDNAs.";
NUCL.POTTOTAL
         RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RR MEDLINE=22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RRA Klausner R.D., Collins F.S., Wagner L., Shensen C.F., Bhat N.K.,

RRA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RRA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RRA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RRA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RRA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RRA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RRA Rahey J., Hélton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RRA Rahey J., Hélton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RRA Rahey J., Hélton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RRA Rahey J., Hélton E., Ketteman M., Madan A., Schierd G.G.,

RRA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RRA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RRA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RRA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RRA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RR
EMBL; AP078752; AAC72917.1; -; mRNA.

EMBL; AK008995; -; NOT ANNOTATED CDS; mRNA.

REMBL; BC003717; AAH037177.1; -; mRNA.

REMBL; BC003717; AAH037177.1; -; mRNA.

REDSembl; EMSMUSG0000002555; Mus musculus.

REDSEMBL; EMSMUSG0000002555; Mus musculus.

REDSEMBL; EMSMUSG0000002555; Mus musculus.

REDSEMBL; ENSMUSG0000002555; Mus musculus.

REDSEMBL; AF00371; DA.

REDSEMBL; AF07299; MBOAT fam.

REDSEMBL; AF07299; MBOAT fam.

REPSOMES; MBOAT; DA.

REPSOMES; MBOAT
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PATHWAY: Central role
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CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol =
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                                 LMYVHDYYVLNYEAP
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                                                                             AELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFL
                                                                                                            QLQVGLIQQMYVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAV
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                                                                   ABLLQFGDREFYRDWWNAES
                                                                                                   QLQVGLIQQWMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWFFHSCLNAV
                                                                                                                                    KKVSGAAAQQAVSYPDNLTYRDLYYFIFAPTLCYELNFPRSPRIRKRFLLRRVLEMLFFT
                                                                                                                                            KKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFT
                                                                                                                                                                              LATILCFPAAVVLLVESITFVGSLLALMAHTILFLKLFSYRDVNSWC--RRARAKAASAG
                                                                                                                                                                                                               GILVDPIQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVAN
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85.1%;
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Pred.
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No. 1.7e-174;
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Q54AA6 M
Q54AA6 M
AC Q54AA6;
DT 13-SEP-2
DT 13-SEP-2
DT 13-SEP-2
DE Diacylg-1
GN Name-Dga
GN Name-Dga
GN Mus musc
OC Eukaryot
OC Muridae;
OC Muridae;
OC MUSTIAE;
Submitted (MAR-2001) to the E
EMBL; AB057816; BAC66171.1; -
MGI; MGI:1333825; Dgat1.
GO; GO:0016021; C:integral to
GO; GO:0005624; C:membrane fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q54AA6 MOUSE PRELIMINARY;
Q54AA6;
Q54AA6;
13-SEP-2005 (TrEMBLrel. 31, I
13-SEP-2005 (TrEMBLrel. 31, I
13-SEP-2005 (TrEMBLrel. 31, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SI
Yamasaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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Name=Dgat1; Synonyms=Dgat;
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                                                                                                                                                                                                                                                          "Mus musculus
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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acyltransferase
                                           membrane;
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SULT 8

WHZ1_PIG
D QBMHZ1;
AC QBMHZ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-EBB-2005 (TrEMBLrel. 29, Last sequence updated)
DT 01-EBB-2005 (TrEMBLrel. 29, Last annotation upd DE Diacylglycerol acyltransferase.

GN Name-DGAT; Synonyms-DGAT1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Verte Mammalia; Eutheria; Laurasiatheria; Cetartic
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...LEOTIDE SEQUENCE.
Pahrenkrug S.C., Smith T.P.L., Fre Vallet J., Wise T., Rohrer G.A., Pt Keele J.;
Submitted (MAY-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 421; Conserv
                                                                   MEDLINE=22351654; PubMed=12464029; Nonneman D., Rohrer G.A.; "Linkage mapping of porcine DGAT1 to contains QTL for growth and fatness." Anim. Genet. 33:472-473(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003846; F:2-acylglycerol O-acyltransferase activity; IDA Acyltransferase; Transferase. SEQUENCE 498 AA; 56790 MW; E7B0DD6DDCF1EC2B CRC64;
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85.1%; Pred. No. 1.7e-174;
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              EMBL/GenBank/DDBJ databases
                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
heria; Cetartiodactyla; Suina; Suida
                               Freking E
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Query Match
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Matches 430
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NORTHERMAN D.J., ROBYET G.A.;

NORTHERMAN D.J., ROBYET G.A.;

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ Submitted (MAY-2002) to the EMBL/GenBank/DDBJ EMBL; AX903557; AAM19083.1; -; mRNA.

EMBL; AX9116586; AAM66767.1; -; Genomic DNA.
GO; GO:0016740; F:transferase activity; IEA
GO; GO:0016740; F:transferase activity; IEA.

InterPro; IPR004299; MBOAT fam.

Pfam; PF03062; MBOAT; 1.
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Nonneman D.J., Rohrer G

Submitted (MAR-2002) to

[4]
acyltransferase).

Name=Dgat1; Synonyms=Dgat;

Rattus norvegious (Rat).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Muroidea; Muridae; Murinae; Rattus.

NCBI TaxID=10116;

[1]
                                                                                                                    RAT STANDARD; PRT; 498 AA. OPERMS; OPERMS; (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
Diacylglycerol O-acyltransferase 1 (EC 2.3.1.20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acyltransferase; Transferase.
SEQUENCE 489 AA; 55814 MW;
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Pred. No. 1.6e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This Swiss-Prot entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstations the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic reticulum (By similarity).
SIMILARITY: Belongs to the membrane-bound acyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COA as substrates.
CATALYTIC ACTIVITY: Acyl-CoA + 1,2-diacylglycerol = CoA
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              AELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFL
                                                                                                                                KKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFT
                                                                                                                                                                    LATIICFPAAVALLVESITPVGSLFALASYSIIFLKLSS
                                                                                                                                                                                                                            GILVDPIQVVSLFLKDPYSWPAPCLIIASNIFIVATFQIEKRLSVGALTEQMGLLLHVVN
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AELLQFGDREFYRDWWNAESVTYFWQNWNI PVHKWCIRHFYKPMLRLGSNKWMARTGVFW
                                                                                                             KKVSGAAAQNTVSYPDNLTYRDLYYFIFAPTLCYELNFPRSPRIRKRFLLRRVLEMLFFT
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No. 1.6e
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Moorley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilking M., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,;
Br.C. Marl and sequences ";
Br.C. Dans C.D. A. Schein J.S., Jones S.J.M., Marra M.A.;
Br.C. Dans C.D. A. Schein J.S., Jones S.J.M., Marra M.A.;
Br.C. Dans C.D. A. Schein J.S., Jones S.J.M., Marra M.A.;
                                                                                                                                                            Query Match
Best Local
                                                                                                                                           Matches
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01-MAR-2004
01-MAR-2004
                                                                                                                                                                                                                                                         Submitted (APR-2001) to the EMBL/GenBahk/DDBJ databases. EMBL; BC006263; AAH06263.4; -; mRNA. GO: GO:0006489; F:electron transporter activity; IEA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR004299; MBOAT fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                              InterPro; IPR004299; I
Pfam; PF03062; MBOAT;
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Name=DGAT1;
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; Pred. No. 1.3e
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RGherration and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Query Match
Best Local Similarity
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JO BRARE
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                                               Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063970; AAH63970.1; -; mENA.
ZFIN; ZDB-GENE-030131-4600; zgc:77691.
Interpro; IPR004299; MBOAT_fam.
pfam; PP03062; MBOAT; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 499 AA; 57151 MW; 3B3E3DA7685AEDF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257;
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ORFNames=zgc:77691;
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                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12477932; DOI=10.1073/pnas.242603899
65.0%;
63.8%;
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Pred.
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1686; DB 2;
No. 7.4e-127;
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                                                AQIAVFFLSAFFHEYLVSVPLKMFRLWAFLGMMLQVPLAILVGRYLRGNYGNAAVWMSLI
                                                                 ARTGVFLASAFFHEYLVSVPLRMFRLWAFTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLI
                                                                                                               HSCLNAVAELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWM
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              IGQPIAVLMYVHDYYVLNYEAPAAEA
                                                                                                LATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWCRRAR-AKAASAGK
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 IGOPIAVLMYVHDYYVLHY-GSASEA
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RA Fahag
RA Fahag
RA Bakk
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RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Tochman J.W., Green E.D., Dickson M.C.,
RA Holkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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Q4RLB7; TETNG PRELIMINARY; PRT; 473 AA.
Q4RLB7;
13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 21 SCAF15022, whole genome shotgun sequen
                                                                                                                                         (Fragment)
ORFNames=GSTENG00032560001;
ORFNames=GSTENG00032560001;
Tetraodon n1groviridis (Green puffer).
Tetraodon; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;
Actinopterygli; Neopterygli; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygli; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ
EMBL; BC076012; AAH76012.1; -; mRNA.
ZFIN; ZDB-GENE-040718-158; zgc:92327.
InterPro; IPR004299; MBOAT_fam.
Pfam; PF03062; MBOAT; 1.
SEQUENCE 507 AA; 58757 MW; AE481F09E0667FF
  NUCLEOTIDE SEQUENCE.
Jaillon O., Aury J.M., Brunet F.
Mauceli E., Bouneau L., Fischer
Nicaud S., Jaffe D., Fisher S.,
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F., Petit J.L., Stange-Thomann er C., Ozouf-Costaz C., Bernot i., Lutfalla G., Dossat C., Segu
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s of more than 15,000
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                                                                                                                                                                                                                                                                                                         shotgun sequence
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       B.
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RESULT 14
QARIJ8 TETNG
QARIJ8 TETNG F
AC Q4RIJ8;
DT 13-SEP-2005 (T
DT 13-SEP-2005 (T
DT 13-SEP-2005 (T
DT 13-SEP-2005 (T
DF (Fragment).
GN ORFNames-GSTEN
OS Tetraodon nigr
OC Eukaryota; Met

13-SEP-2005 (TrEMBLrel. 13-SEP-2005 (TrEMBLrel. 13-SEP-2005 (TrEMBLrel. Chromosome 8 SCAF15044,

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PRELIMINARY;

ORFNames=GSTENG00034052001; Tetraodon nigroviridis (Green Eukaryota; Metazoa; Chordata;

puffer). Craniata;

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Matches 301; Conserv
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NON_TER
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Genoscope; Whitehead Institute Centre for Genome Rese
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databas
-!- CAUTION: The sequence shown here is derived from
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entr
preliminary data.
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                                                                                                AFTGMMAQIFLAWFVGRFFQGNYGNAAVWLSLIIGQFIAVLMYVHDYYVLNY
                                                                                                                                                                                                                                             PFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSES
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                                                                                                                                                                                                               PFQEMNFSRMVERLLKLAVPNHLIWLIFFYWFFHSSMNFVAELLQFGDREFYKDWWNSET
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No. 6.
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SQUE COCCORRENCE READER READER

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RESULT 15
Q91YB5_RAT
ID Q91YB5_RAT
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RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Cruaud C., Duprat S., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Laudet V., Schachter V., Ouetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
The early vertebrate proto-karyotype.";
U. Nature 431:946-957(2004).
UN [2]
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Best Local S
Matches 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILCFPAAVVLLVE
|:||| ||| ||| :| |:|:|:|:||:|||||||:
PYSWPAACLVIVANVFVLVALYTERQLSXGSFSERVGCLIHCVNWAVLITFPAAVVLLLP
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                                                                                                                         SLIIGQPIAVLMYVHDYYVLNYEAPA
                                                                                                                                                                                                        FHBYLVSVPLRMFRLWAFTGMMA------
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                                                                                                                                                                                FHBYLVSVPLRMFRLWAFMGMIAQWKVGFDNIDSSHHQIPLAWFVGRFLRGNYGNAAVWI
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447 AA;
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Pred. No. 1.2e
52; Mismatches
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..2e-120;
les 70;
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STRAIN-Wistar; TISSUE-Liver;

STRAIN-Wistar; TISSUE-Liver;

Waterman I.J., Zammit V.A., Price N.T.;

EMBL; AJ345014; CAC69884.1; -; mRNA.

GO; GO:0008415; F:acyltransferase activity; IEA.

GO; GO:0004144; F:diacylglycerol O-acyltransferase actorious (GO; GO:0016740; F:transferase activity; IEA.

InterPro; IPR004299; MBOAT_fam.

Pfam; PF03062; MBOAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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01-DEC-2001 (TrEMBLrel. 19, Last
01-JUN-2003 (TrEMBLrel. 24, Last
01-JUN-2003 (TrEMBLrel. 24, Last
Diacylglycerol acyltransferase I
Name=dgati;
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NON_TER 1 1
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SEQÜENCE 242 AA; 29014 MW;
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nilarity 92.5%;
Conservative
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r treating hyperlipidemia, atherosclerosis, heart disease, or of seases associated with an imbalance of triglyceride levels. seases associated with an imbalance of triglyceride levels. aim 1; Fig 1A; 32pp; English. e enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1) recomposed acyltransferase 1 (ACAT1) recomposed acyltransferase (DGAT). The present sequence is human ACAT Related Gene Producestasis. The present sequence is human ACAT Related Gene Producestasis. The present sequence is thought therefore that recomposed cost ont esterify cholesterol. It is thought therefore that ricipates in the Coenzyme A-dependent acylation of substrate(s) and cholesterol e.g. diacylglycerol. Also, ARGP1 has a predicted acylglycerol binding motif, suggesting that it may perform the lacylglycerol binding motif, suggesting that it may perform the	-OCT-1998; 98US-00165042. PYCO) UNIV COLUMBIA NEW YORK. Urley SL, Oelkers P; T; 2000-557622/51. PSDB; AAA76169. W nucleic acid encoding a human diacylglycerol acyltransferase	XX XX XW Acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1; Sterol esterification; lipid homeostasis; diacylglycerol acyltransferase XM XM XM XM XM XM XM XM XM X	1 00 0815200 standard; protein; 488 0815200;	25 2046 78.9 387 8 ADQ39677 26 2039 78.6 386 3 AAY44561 Aay44561 Human Dia Ady39679 1681 64.8 421 8 ADH35335 ENZM prot 28 1681 64.8 421 8 ADG39679 Adg39679 Adg39679 1681 64.8 421 8 ADG39679 Adg39679 Adg39679 Adg39679 Adg39679 Human myo 29 1297 50.0 236 5 ABB60791 Abb610191 Human Dia Abg6778 Human pol 29 29 29 29 29 29 29 29 29 29 29 29 29

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Pred. No. 2.4e-273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a compound targeted to a nucleic acid molecule encoding diacylglycerol acyltransferase 1. The compound is useful for treating a disease or condition associated with diacylglycerol acyltransferase 1; modulating glucose or cholesterol levels, or lowering triglyceride levels in an animal; or for delaying the onset of a disease or condition associated with diacylglycerol acyltransferase 1 in an animal, such as abnormal lipid metabolism, abnormal cholesterol metabolism, atherosclerosis, abnormal metabolic condition, hyperlipidaemia, diabetes, type 2 diabetes, obesity, cardiovascular disease. The present sequence represents the amino acid sequence of human diacylglycerol acyltransferase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides targeted to diacylglycerol acyltransferase
1, useful for treating diacylglycerol acyltransferase 1-associated
diseases or conditions, e.g. atherosclerosis, hyperlipidemia, diabetes or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                  VSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILCFPA
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                                    VPLRMFRLWAFTGWMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLN
                                                       VSYPDNLTYRDLYYFLFAPTLCYELNFPR9PRIRKRFLLRRILEMLFFTQLQVGLIQQWM
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Pred. No. 2.4e-273;
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RESULT 3
ADS84845
ID S84845
AC ADS8
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                                                                                                                                                                                                         The invention describes a compound 8 to 80 nucleobases in length targeted CC to a nucleit acid molecule encoding diacylglycerol acyltransferase 1 CC (DGAT1), where the compound specifically hybridises with the nucleic acid comolecule encoding DGAT1 comprising a sequence comprising 1976 by (SEQ ID CC NO: 4) fully defined in the specification, and inhibits the expression of DGAT1. Also, described are: inhibiting the expression of DGAT1 in cells or ctissues; sefeening for a modulator of DGAT1; a diagnostic method for CC compound above; modulating glucose levels in an animal; preventing or CC clarifying, a disease state; a kit or assay device comprising the CC compound above; modulating glucose levels in an animal; preventing or CC delaying the onset of a disease or condition associated with DGAT1 in an CC animal; modulating cholesterol levels in an animal; reducing serum CC glucose levels, DGAT1 levels in the liver, circulating insulin levels, conglucose tolerance tests and insulin tolerance tests, reducing CC circulating triglycerides, liver triglycerides or free fatty acids in the CC compound is useful in a method for treating an animal having a disease or condition associated with DGAT1, i.e., abnormal lipid metabolism, CC condition associated with DGAT1, i.e., abnormal lipid metabolism, CC condition (l.e., hyperlipidaemia), diabetes (i.e., Type 2 diabetes), observe, or cardiovascular disease, so that expression of DGAT1 is conhibited. This is the amino acid sequence of human diacylglycerol
Query Match
Best Local Similarity
Matches 488; Conserv
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                                                                                                                               Sequence 488
                                                                                                                                                                                           inhibited. This is the ami acyltransferase 1 (DGAT1).
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N-PSDB; ADS84617.
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                     GENBANK;
                                 WPI; 2003-268312/26.
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CC The sequence data for this patent did not form part of the printed constricted as obtained in electronic form directly from WIPO at the constriction will the printed in the constriction will be a constriction of the printed constriction and constriction is patent did not form directly from WIPO at the specification, which is defined to the constriction will be a construction of the printed constriction will be a construction of the printed constriction will be a construction of the construction will be a construction of the cons
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Query Match Best Local Similarity

99.8**%;** 99.8**%**;

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                                                                                                  The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, cc derivative or allelic variation of the nucleic acid sequence. Also cc claimed are a vector comprising the novel polynucleotide, a host cell cc which is differentially regulated in an animal subjected to pain and a cc kit to perform the method, an array, a method for identifying a nucleotide sequence that is differentially expressed in neuronal tissue of a first animal cc the expression of the polynucleotide sequence the expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for pain, a method for identifying a pharmaceutical composition, a cc method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides or their antibodies. The polynucleotide given in the specification, a method for identifying a compound useful in treating composition composition composition composition composition composition or polypeptides or their antibodies. The polynucleotide or the compound that compound that segmental nerve injury (Chung), chronic constriction compile the one or more of the polypeptides or their antibodies. The polynucleotide or the compound that the polypeptides or their antibodies. The polynucleotide or the constriction compile and the polypeptides or their antibodies. The polynucleotide or the constriction constriction injury (CC1) and sparted nerve injury (SNI) in an animal (e.g. gene constriction which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed constriction by the polypeptide or the constriction of the printed constriction in t
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Sequence
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WPI; 2004-347921/32.
N-PSDB; ACN38859.
                                                                                                                02-OCT-2002; 2002US-0414971P
                                                                                                                                               29-SEP-2003,
                                                                                                                                                                                  15-APR-2004
                                                                                                                                                                                                             WO2004030615-A2
                                                                                                                                                                                                                                                                                               cervical cancer; melanoma; leukaemia; chromosome identification; chromosome
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New tumor-associated antigenic target polypeptides and nucleic useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian prostate cancer or tumor. o R acids,

The invention relates to human tumour-associated antigenic target (TAT) CC polypeptides, and their related mucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and colypeptide; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic complexity and methods and compositions for the treatment or composition serve are useful for diagnosis of cancer in mammals. TAT polypeptides, nucleic acids and compositions are useful for diagnosis of cancer in mammals. TAT polypeptides nucleic acids cantibodies, antipodies, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovariah cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and lenkaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence

VPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREF VPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVABLMQFGDREF VSYPDNLTYRDLYYFLFAPTLCYELNFPR&PRIRKRFLLRRILEMLFFTQLQVGLIQQWM AVVLLVESITPVGSLLALMAHTILFLKLF6YRDVNSWCRRARAKAASAGKKASSAAAPHT VSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILCFPA SGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDPIQV MGDRGSSRRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAPNKDGDAGVG YRDWWNSESVTYFWQNWNI PVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVS YRDWWNSESVTYFWQNWNI PVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVS AVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWCRRARAKAASAGKKASSAAAPHT VSLFLKDPYSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILCFPA SGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDPIQV MGDRGSSRRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAPNKDGDAGVG RDLYYFLFAPTLCYELNFPR6PRIRKRFLLRRILEMLFFTQLQVGLIQQWM Score 2588; DB 8; Pred. No. 1.1e-272; 1; Mismatches 0; Length Indels 488; 0 Gaps 480 480 420 360 360 300 240 180 180 120 420 300 240 120 60 6

240

120

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CC the specification or its complement and encoding any one of the amino card sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding comprising an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in the coolynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid, comprising the coolynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a mucleic acid molecule; a method of detecting a variant polypeptide; and a composition for identifying an agent useful in treating or preventing composition is useful in identifying an individual who has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This sequence represents the protein of a human myocardial infarction. Note: This sequence was not shown in the specification. The sequence has come from the wipo website.
                                          Query Match
Best Local S
                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-2002; 2002US-0434178P.
10-MAR-2003; 2003US-04531359.
30-APR-2003; 2003US-046412P.
23-SEP-2003; 2003US-0504955P.
                                                                                          Sequence 488
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                          Local Similarity 99.0 nes 487; Conservative
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                                                                                                                                                                                          20-DEC-2002;
10-MAR-2003;
30-APR-2003;
23-SEP-2003;
             Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ39678 standard; protein; 488
                                                                              N-PSDB;
                                                                                              WPI; 2004-533949/51.
                                                                                                                          Cargill M,
                                                                                                                                                                                                                                                                         22-DEC-2003; 2003WO-US040978
                                                                                                                                                                                                                                                                                                         15-JUL-2004.
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                    cardiant; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                    Myocardial infarction; detection; single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human myocardial infarction-associated gene derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSLFLKDPYSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILCFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDPIQV
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                                                                                                                                                                                        ; 2002US-0434778P.
; 2003US-0453135P.
; 2003US-0466412P.
; 2003US-0504955P.
                                                                                                                          Devlin JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488
                                                                                                                              Iakoubova
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein, SEQ ID 1341.
                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphism; SNP;
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480 480 420 420 360 360 300 300

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MGDRGSSRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAPNKDGDAGVG

60

in

Claim 10;

SEQ

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NO 1341; 145pp; English

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The invention relates to a novel method for identifying an individual who CC comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's CC nucleic acids, where the presence of the SNP is correlated with an CC altered risk for myocardial infarction in the individual's CC nucleic acids, where the presence of the SNP is correlated with an CC altered risk for myocardial infarction in the individual's CC contiguous nucleotides where one of the nucleotides is an SNP given in the specification; an isolated polypoptide comprising at least CC comprising an amino acid sequence given in the specification, an antibody that specifically binds to the polypoptide or its antigen-binding CC fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in CC length; a kit for detecting an SNP in a nucleic acid molecule; a method of detecting a SNP in a nucleic acid molecule; a method of detecting a variant polypoptide; and a comprising the infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The CC method is useful in identifying an individual who has an increased or composition for treating or preventing myocardial infarction. This compositated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from CC sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
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                                                                                                                                                                                                                                                                           YRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGDRGSSRRRRTGGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAPNKDGDAGVG
YEAPAAEA 488
                                                           YEAPAAEA 488
                                                                                                                                                                                                                                           YRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVS
                                                                                                                                                                                                                                                                                                                                                             VPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREF
                                                                                                                                                                                                                                                                                                                                                                                               VPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFTQLQVGLIQQWM
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                                                                                                                       VPLRMFRLWAFTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGDRGSSRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPANKDGDAGVG
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Pred. No. 1.1e-272;
Pred. No. 1.1e-272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 488;
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--NKDGDAGVGSGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLI MGDRGGAGSSRRRTGSRVSIQGGSGPMVDEEEVRDAAVGPDLGAGGDAPAPAPVPAPAH MGDR----GSSRRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAP-----

109 60 51 ω ,

427;

Conservative

Indels

13;

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The present sequence represents an acyl-CoA:cholesterol acyltransferase (C (ACAT) related protein. The ACAT-like protein is active in the formation of a sterol, ester and/or triacylglycerol from a fatty acyl-CoA and CC sterol and/or diacylglycerol substrate. The DNA can be used for modifying CC the lipid composition of plant cells. The ACAT-like protein has CC diacylglycerol acyltransferase (DAGAT) activity, and so the synthesis of CC triglycerides can be suppressed or increased using the DNA. The protein CC may be used to produce plant oils with, a modified triglyceride content. CC me products can also be used to identify antagonists and agonists of CC DAGAT activity. Such agonists and antagonists are particularly useful in CC treating or ameliorating diseases associated with DAGAT activity. CC including diseases associated with altered cellular diacylglycerol CC cardiopulmonary diseases e.g. heart failure, atherosclerosis, and diseases associated with abnormal lipid metabolic and diseases associated with abnormal lipid metabolism, and diseases associated with abnormal lipid metabolism.
Query Match
Best Local S
Matches 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developing products for treating e.g. disease or metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acyl-CoA:cholesterol acyltransferase; ACAT; ACAT-like protein; sterol; ester; triacylglycerol; fatty acyl-CoA; lipid composition; plant cell; diacylglycerol acyltransferase; DAGAT; triglyceride; cancer; diabetes; cardiopulmonary disease; heart failure; atherosclerosis; adipocytosis; leukaemia; skin carcinoma; fibroblastoma; metabolic disorder; obesity; abnormal lipid metabolism; abnormal fat absorption;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 11; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polynucleotides used for modifying plant oil composition and for developing products for treating e.g. cancer, diabetes, cardiopulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ45385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1998;
12-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY54139 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-105701/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lassner MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CALJ ) CALGENE LLC
                Similarity
                                                                     500 AA;
                                                                                                       and adipogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           secretion; adipogenesis.
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                88.6%;
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Score 2299.5; DB 3
Pred. No. 3.4e-241;
6; Mismatches 31;
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RESULT 10
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AAB19742
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AC AAB15
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AAAB19742
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AC AAB16
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AC ACA
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The present sequence is that of rat acyl CoA:cholesterol acyltransferase (ACAT), as deduced from ACAT DNA (see AAA88846). Sterol O-acyltransferases such as ACAT catalyse the formation of cholesterol
                                                                                              Disclosure; Page 64; 166pp; English
                                                                                                                                                                 Genetically engineering the biosynthetic pathways in plants involved in the accumulation of sterol compounds and tocopherol to produce compounds for lowering the level of low density lipoprotein cholesterol in blood
                                                                                                                                                                                                                                                                  WPI; 2000-665136/64
N-PSDB; AAA88846.
                                                                                                                                                                                                                                                                                                                                                              Venkatramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-2000
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tocopherol; phytosterol; phytostanol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2001
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                                                                                                                                                                                                                                                                                                                                       Kishore
                                                                                                                                                                                                                                                                                                                                                                                                             (MONS ) MONSANTO
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Lardizabal
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Lassner MW,
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W, Rangwala SH,
                                                                                                                                                                                                                                                                                                                                       Grebenok RJ;
Karunanandaa
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ELASAFFHEYLVSIPLRMFRLMAFTAMMAQVPLAWIVNRFFQGNYGNAAVWVTLIIGQPV
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AVLMYVHDYYVLNYDAP
                                                                                                                             AVABLMOFGDREFYRDWWNSESVTYFWONWNIFVHKWCIRHFYKPMLRRGSSKWMARTGV
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                          AVLMYVHDYYVLNYEAP
                                                                                                                                                                     FTQLQVGLIQQWMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLN
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Pred. No. 3.4e-241;
6; Mismatches 31;
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RRSULT 11
AAE24973
ID AAE24973;
XX
XX
AAE24973;
XC AAE24973;
XX
DT 22-OCT-2002 (first entry)
XX
DE Bovine DGAT1 protein.
XX
KW Bovine; diacylglycerol acyltransferase; genotyping; milk production;
XX
DGAT1; polymorphism; farming industry; transgenic; chromosome 14; enzyme.
XX
DS Bos taurus.
XX
PN WO200236824-A1.
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WO200236824-A1.
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10-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                    CC The invention relates to a method of genotyping bovine for improved milk CC production traits which comprises determining the diacylglycerol CC acyltransferase (DGAT1) genotypic state of the bovine, wherein the DGAT1 CC gene and polymorphisms have been found to be associated with such CC improved milk production traits. The method is useful for selecting a CC bovine having a desired DGAT1 genotypic state. It is also useful for the CC ints DGAT1 gene. Milk produced from selected bovine which is useful for CC making a dairy product provides a beneficial health effect. An antibody to the protein having DGAT1 activity is useful for inhibiting the CC cotivity of bovine DGAT1 in a lactivity is useful for inhibiting the CC generate transgenic animals which are useful to investigate the molecular DGAT1 action and to test a substance for the ability to prevent, CC basis of DGAT1 action and to test a substance for the ability to prevent, CC slow or enhance DGAT1 activity. The present sequence is bovine DGAT1

CC protein. DGAT1 gene is located on chromosome 14
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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(COPP/)
(GRIS/)
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COPPITTERS W H
GRIBART B M J.
SNELL R G.
REID S J.
FORD C A.
SPELMAN R J.
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, Spelman
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                 GLIQQWMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELM
                                                                          SAÅAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFTQLQV
GLIQQWWVPAIQNSMKPFKDMDYSRIVERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELM
                                                       GGAAQRTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRLLEMLFLTQLQV
                                                                                                                 FPAAVAFILESITPVGSVLALMVYTILFLKLFSYRDVNLWCRERRAGAKAKAALAGKKAN
                                                                                                                                              FPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWCRR----ARAKAASAGKKAS
                                                                                                                                                                           IQVVSLFLKDPYSWPALCLVIVANIFAVAAFQVEKRLAVGALTEQAGLLLHGVNLATILC
                                                                                                                                                                                                      IQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILC
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Pred. No. 1.9e
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(COPP/)
(GRIS/)
(SNEL/)
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06-DEC-2000;
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Synthetic.
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SNELL R G.
REID S J.
FORD C A.
SPELMAN R J
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, Spelman
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The invention relates to a method of genotyping bovine for improved milk production traits which comprises determining the diacylglycerol acyltransferase (DGAT1) genotypic state of the bovine, wherein the DGAT1 gene and polymorphisms have been found to be associated with such improved milk production traits. The method is useful for selecting a bovine having a desired DGAT1 genotypic state. It is also useful for the identification and selection of a bovine having one of the polymorphisms in its DGAT1 gene. Milk produced from selected bovine which is useful for making a dairy product provides a beneficial health effect. An antibody to the protein having DGAT1 activity is useful for inhibiting the

Page; 128pp; English.

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ABP960 ID ABP96
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity of bovine DGAT1 in a lactating bovine so as to modulate milk production and/or milk solids content. DGAT1 nucleic acid and its fragments are useful in the farming industry. They are also useful to generate transgenic animals which are useful to investigate the molecular basis of DGAT1 action and to test a substance for the ability to prevent, slow or enhance DGAT1 activity. The present sequence is bovine DGAT1 protein mutant used to illustrate the method of the invention. Note: This sequence is not shown in the specification, however it is constructed based on the sequence SEQ.ID.NO:2 shown in the sequence listing (AAE24973)
                                                                               Acyl CoA:diacylglycerol transferase; DGAT; milk; meat marbling; low fat; polymorphic; single nucleotide polymorphism.
 16-JAN-2003
                            WO2003004630-A2
                                                        Bos taurus
                                                                                                                                       Bovine DGAT protein SEQ
                                                                                                                                                                   07-MAY-2003
                                                                                                                                                                                                                        ABP96046 standard;
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                                                                                                                                                                                                                                                                                            HDYYVLNREAPAA
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                                                                                                                                                                                                                                                                                                                                                                                                       QFGDREFYRDWWNSESITYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWAARTAVFLASAF
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                                                                                               enzyme; chromosome 14; bovine, SNP;
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GLIQQMMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELM

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55

DVGSGHWNLRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDP

114

IQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILC 177 IQVVSLFLKDPYSWPALCLVIVANIFAVAAFQVEKRLAVGALTEQAGLLLHGVNLATILC

178

PPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWCRR----ARAKAASAGKKAS 233

YRDVNLWCRERRAGAKAKAALAGKKAN

234

294 353

5

Matches

433;

Conservative

14;

Query Match Best Local Similarity

87.8%;

Score 2278.5; DB 6 Pred. No. 6.4e-239; [4; Mismatches 33;

6;

Indels Length

13;

Gaps

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The present invention describes a nucleic acid molecule (NA) (I) encoding CC abovine acyl CoA-diacylglycerol transferase (DAAT) contributing to or cindicative for low fat content of milk and to low meat marbling CC (intramuscular fat content). Human DAAT is located to chromosome 8, and bovine DAAT is located to chromosome 8 and CC mammal for its predisposition for fat dontent of milk and/or its useful for testing a CC mammal for its predisposition for fat dontent of milk and/or its cencoding DAAT for nucleotide polymorphisms (e.g. single nucleotide polymorphisms (sNPs)) which are connected with the predisposition. The CC polymorphisms (sNPs)) which are connected with the predisposition of an amino CC gene and result in substitution, deletion and/or addition of an amino CC gene and result in substitution, deletion and/or addition of an amino CC gene a quanine and a cytosine which is encoded by the gene. The CC guanine, 11030 a guanine, 11048 a cytosine or thymine and 10434 of the DGAT CC gene a quanine and a cytosine residue, at position 3343 a cytosine or thymine and 1093 a cytosine or thymine and low meat marbling. The nucleid acid molecule has a the position of corresponding to position 1043 and 10434 of the DGAT gene two adenine corresponding to position 1043 and 10434 of the DGAT gene two adenine cytosine or the position for high content of milk and cytosine or the position of the DGAT gene two adenine cytosine or the position of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid molecule comprising a sequence of an allele of a polymorphic bovine acyl CoA-diacylglycerol transferase gene useful testing a mammal for its predisposition for fat content of milk and
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 90-91; 91pp; English
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2002US-0379412P.
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RESULT 14
ADC16606
AD ADC16
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XX lipop
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                    CC This invention relates to novel diacylglycerol O-acyltransferase CC (diglyceride acyltransferase; DGAT; EC 2.3.1.20) nucleotide and protein CC sequences. The DGAT enzyme is involved in triacylglycerol synthesis, and CC is important in higher eukaryotes for intestinal fat absorption, CC is important in higher eukaryotes for intestinal fat absorption, and CC possibly egg production and sperm maturation. The DGAT nucleotide CC sequences may be useful for identifying DGAT homologues, as a source of compose and primers, for the identification of expression patterns in CC probes and primers, for the preparation of cell or animal models of CC probes and frincerion, and for the preparation of models of CC probes and for the preparation of in vitro models of CC function. The invention may also be used for diagnostic screening, for the treatment of pathological conditions, and for treatment of conditions conclude hyperlipidaemia, cardiovascular diseases diagnosed and/or treated concer, neurological disorders and immunological disorders. DGAT may also be administrated to DGAT expression or activity. Diseases diagnosed and/or treated concer, neurological disorders and immunological disorders. DGAT may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diacylglycerol v-acylticus fat absorption; triacylglycerol synthesis; intestinal fat absorption; triacylglycerol synthesis; intestinal fat absorption; lipoprotein assembly; fat storage in adipocytes; milk production; egg production; sperm maturation; hyperlipidaemia; cancer; neurological disorder; industrial disorder; sperm count; transgenic plant; industrial feedstock; transgenic animal; anti-obseity; cardiant; industrial feedstock; transgenic mouse; murine; enzyme; EC 2.3.1.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 5; 63pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel diacylglycerol O-acyltransferase polynucleotides and polypeptides used in treatment therapies and production of triacylglycerols.
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09-NOV-1998;
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DB; ADC16605.
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RESULT 15 ADS00390

standard;

protein;

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Mouse diacylglycerol acyltransferase 1.

ADS00390 st; ADS00390; 16-DEC-2004

(first entry)

Antiarteriosclerotic; Antilipemic; Antidiabetic; Anorectic; Cardiant; Diacylglycerol-Acyltransferase-Inhibitor-1; diacylglycerol acyltransferase 1; glucbse; cholesterol; triglyceride; lipid metabolism; cholesterol metabolism; atherosclerosis; hyperlipidaemia; diabetes; type 2 diabetes; obesity;

cardiovascular disease; mouse;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consumption by humans, or for use as industrial feedstocks. Transgenic animals with altered levels of DGAT can be used as sources for a variety of different food and industrial products in which the triglyceride content is specifically tailored. The invention may enable development of anti-obesity, cardiant, cytostatic or antilipaemic compounds. The present sequence is that of the mouse DGAT protein of the invention. Note: The present sequence does not appear in the specification but was obtained by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence does not
the indexer from GenBank.
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                                                                                                                                                                                                                                                                                                       LATIICFPAAVALLVESITPVGSVFALASYSIMFLKLYSYRDVNLWCRQRRVKAKAVSTG
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                                                                                                                                          AELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFL
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                                                                                                                                                                                                                                                                 KKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFT
                                                                                                                                                                                                                                                                                                                                                                 GILVDPIQVVSLFLKDPYSWPAPCVIIASNIFVVAAFQIEKRLAVGALTEQMGLLLHVVN
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Pred. No. 6.6e-239;
9; Mismatches 34;
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N-PSDB; ADS00247.
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useful for treating diacylglycerol acyltransferase 1-associated
eases or conditions, e.g. atherosclerosis, hyperlipidemia, diabetes or
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                                                                                    ASAFFHEYLVSVPLRMFRLWAFTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAV
                                                                                                                                                                 AELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFL
                                                                                                                                                                                                                                               QLQVGLIQQWMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAV
                                                                                                                                                                                                                                                                                                                          KKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFT
                                                                                                                                                                                                                                                                                                                                                                                    LATIICFPAAVALLVESITPVGSVFALASYSIMFLKLYSYRDVNLWCRQRRVKAKAVSTG
                                                                                                                                                                                                                                                                                                                                                                                                        LATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWC--RRARAKAASAG
                                                                                                                                          ABLLQFGDREFYRDWWNAESVTYFWQNWNIPVHKWCIRHFYKPMLRHGSSKWVARTGVFL
                                                                                                                                                                                                                         QLQVGLIQQWMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWFFHSCLNAV
                                                                                                                                                                                                                                                                                                     KKVSGAAAQQAVSYPDNLTYRDLYYFIFAPTLCYELNFPRSPRIRKRFLLRRVLEMLFFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graham MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8;
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GenCore version 5.1.7

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 12:29:50; Search time 41 Seconds
(without alignments)
1145.214 Million cell updates/sec

Title: US-10-659-800-6
Perfect score: 2594
Sequence: 1 McDRGSSRRRRTGSRPSSHG.......VLMYVHDYYVLNYEAPAAEA 488
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: PIR 80:*
1: Dir1:*
2: Dir1:*
3: Dir1:*
3: Dir1:*
4: Dir4:*
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
90	90.5	90.5	90.5	90.5	90.5	91.5	92.5	93	93	93	94.5	94.5	94.5	95	95.5
ω .5	ω	ω 5	ω .5	ω .5	ω .5	ა ა	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.7	3.7
659	2410	1911	600	395	299	403	287	932	572	416	583	457	228	436	807
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
T33557	T43731	T43048	T11889	B96610	F75060	AF1536	B75155	S09151	I39369	C65183	T19839	T11283	D70358	JQ1459	A34581
hypothetical prote	cell wall alpha-gl	calcium channel al	NADH2 dehydrogenas	hypothetical prote	probable hydrogena	Tetracycline resis	hypothetical prote	suvar(3)7 protein	alpha-1A-adrenergi	hypothetical 45.0	hypothetical prote	NADH2 dehydrogenas	hydrogenase (EC 1.	Bt1 protein precur	oxysterol-binding

ALIGNMENTS

Ş	₽ &	B 4	da d	8 8 8	Query Best Matcl	A;Cross-refi A;Experimen C;Genetics: A;Gene: CES: A;Map posit: A;Introns: I C;Superfami C;Keywords:	A; Referen A; Accessi A; Status A; Molecul	A; Recession A; Accession A; Status: p; A; Molecule t A; Residues: A; Cross-ref A; Experiment B; Dobson B	RESULT 1 T19027 probable ster C;Species: Ca C;Species: Ca C;Accession: R;Kershaw, J: Submitted to
237APHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILE 284	183 VLLVESTTEVGSLIALMAHTILETIKLESTRUVNSWCKKARKAASAGKKASSAA 236	EHHYSIWSWPNLALILCSNIQILSVPGWEXILERGWLGNGFAAVPYTSLVIAHLTIPVVV		6 SSKKKTISKESSNIGGISFARALEEVKLAAAGFUVGAAGJAFAFAFNKGJAAGGAGGISKESSNIGGISFARAEESKKLAAAGFUVGAAGJAFAFAFNKGJAAGGAGGISKESSNIKE 65	42.6%; Score 1106; DB 2; Length 496; Similarity 43.7%; Pred. No. 2.2e-83; O; Conservative 89; Mismatches 155; Indels 40; Gaps	A;Cross-references: UNIPARC:UPI000007P625; EMBL:Z92835; PIDN:CAB07399.1; GSPDB:GN00023; A;Experimental source: clone H19N07 C;Genetics: A;Gene: CESP:H19N07.4 A;Map position: 5 A;Introns: 5/3; 43/2; 77/3; 139/1; 171/3; 456/1 C;Superfamily: sterol O-acyltransferase C;Keywords: acyltransferase; coenzyme A	. 4 9 8 6 4 5	A;Reterence number: 219051 A;Recession: T19027 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-496 <wil> A;Residues: 1-496 <wil> A;Cross-references: UNIPROT:045245; UNIPARC:UPI000007F625; EMBL:Z75526; PIDN:CAA99773.1 A;Experimental source: clone C06H2 R:Dobson R</wil></wil>	RESULT 1 T19027 probable sterol O-acyltransferase (EC 2.3.1.26) H19N07.4 - Caemorhabditis elegans C;Species: Caemorhabditis elegans C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Abate: 15-Oct-19027; T23106 C;Accession: T19027; T23106 R;Kershaw, J. R;Kershaw, J. R;Kershaw, J. R;Kershaw, J. R;Kershaw, J. R;Kershaw, J.

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A;Pathway: triacylglycerol biosynthesis
C;Keywords: acvltranafarana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Cloning of a cDNA encoding diacylglycerol acyltransferase A,Reference number: Z26127 A,Accession: T52584
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R;Hills, M.J.; Lu, C.; Ho
FEBS Lett. 452, 145-149,
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A; Residues: 1-520 < HIL>
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                                 HLIWLIFFYWLFHSCLNAVAELMOFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFY
                                                                             TGVFLASAFFHEYLVSVPLRMFRLWAFTGMMAQIPLAWFVGRFFQ-GNYGNAAVWLSLII 463
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                                                                                                                                                  YDIRS-----LANAADKANP-----EVSY--YVSLKSLAYFMVAPTLCYQPSYPRSA 304
                                                                                                                                                                                                                   QKYISEPVVIFLHIIITMTEVLYPVYVTLRCDSAFLSGVTLMLLT-CIVWLKLVSYAHTS
                                                                                                                                                                                                                                                   VGALTEQAGLLLHVANLATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYR---
                                                                                                                                                                                                                                                                                      IAVNSRLIIENLMKYGWLIRTDFWFSSRSLRD---WPLFMCCISLSIFPLAAFTVEKLVL
                                                                                                                                                                                                                                                                                                           ILSNARLFLENLIKYGILV-DPIQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLA 155
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5-149, 1999
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84576
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A; Map position: 2
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A;Molecule type: DNA
A;Residues: 1-441 <STO>
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                                                                                                                                                                                                                        LIWLIFPYWLFHSCLNAVABLMQFGDREFYRDWWNSESVTYFWQNWNIFVHKWCIRHFYK 391
                                                                                                                                                                                                                                                                                             IRKRFLLRRILEMLFFTQLQVGLIQQWVVPTIQNSMKPFK-DMDYSRIIERLLKLAVPNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILSNARLFLENLIKYGILVDPIQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAV 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGDNNGGGRGGGGGGRGNADATFTYRPSVPAHRRARESPLSSDAIFKQSHAGLFNLCVVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPCLRSKIPKTLAIIIAFĹVSAVFHELCIÁVPCRLFKLWAFLGIMFQVPLV-FITNYLQE
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                                                                                                                                                                                                                                                                                                                                         DIRS-----LANAADKANP-----EV9Y--YVSLKSLAYFMVAPTLCYQPSYPRSAC
                                                                                                                                                                                                                                                                                                                                                                         DVNSWCRRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPR
                                                                                                                                                                                                                                                                                                                                                                                                            ------LSGVTLMLLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                          GALTEQAGLLLHVANLATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPNKDGDAGVGSGHWELRC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLRRKSRSDSSNGLLLSGSDNNSPSDDVØAPADVRDRIDSVVNDDAQG-TANLAGDNNG
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                                                                  -GNMIFWFIFCIFGQPMCVLLYYHD
                                                                                                  YGNAAVW-LSLIIGQPIAVLMYVHD 475
                                                                                                                                    PCLRSKIPKTLAIIIAFLVSAVFHELCIAVPCRLFKLWAFLGIMFQV---
                                                                                                                                                                  PMLRRGSSKWMARTGVELASAFFHEYLVSYPLRMFRLWAFTGMMAQIPLAWFVGRFFQGN
                                                                                                                                                                                                                                                                        IRKGWVARQFAKLVIFTGFMGFIIEQYINPIVRNSKHPLKGDLLYA--IERVLKLSVPNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 661/ DB 2;
Pred. No. 9.7e-47;
1; Mismatches 137
                                                                                                                                                                                                                                                                                                                                                                                                              ----IVWLKLVSYAHTSY 198
                                                                    432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----HRLQDSLFSSDSGF-SNYRGILNWCVVML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPAAAEEE----VRDAAAGPDVGAAGDAPA
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-194, 78, 196-540 <GRE>
A; Cross-references: UNIDARC: UPT0000170CD5; GB:S81092; NID:g1478335; PIDN:AAB36050.1;
A; Experimental source: peritoneal macrophages
C; Comment: This enzyme helps maintain cellular cholesterol homeostasis by catalyzing
y cholesterol and oxygenated sterols.
C; Genetics:
A; Gene: ACACT
A; Map position: 1
C; Superfamily: sterol O-acyltransferase
C; Keywords: acyltransferase; cholesterol; coenzyme A; endoplasmic reticulum; transmen
                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA,
A; Residues: 1-540 <-RES
A; Cross-references: UNIPROT: Q61263; UNIPARC: UPI000002816F; GB: L42293; NID: g1066809; PIDN
R; Green, S.; Steinberg, D.; Quehenberger, O.
Biochem. Biophys. Res. Commun. 218, 924-929, 1996
Biochem. Biophys. Res. Commun. 18, 924-929, 1996
A; Title: Cloning and expression in Xenops oocytes of a mouse homologue of the human acy
A; Reference number: JC4617; MUID: 96158986; PMID: 8579615
A; Accession: JC4617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1:
C;Accession: 149454; JC4617
R;Uelmen, P.J.; Oka, K.; Sullivan, M.C.; Chang, J. Biol. Chem. 270, 26192-26201, 1995
A;Title: Molecular cloning of mouse ACACT.
A;Reference number: 149454; MUID:96084687; PMID
A;Accession: 149454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence A;Reference number: Z14177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sterol O-acyltrahsferase homolog F27F23.26 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: T01294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: acyl-coenzyme A cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sterol O-acyltransferase (EC 2.3.1.26) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   문
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A; Residues: 1-231 < ROU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Mus musculus (house mouse)
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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;Introns: 44/3; 70/3; 104/3; 150/2; 177/3; 184/3; 205/3
;Note: F27F23.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 4.6e-31;
2; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMID:7592824
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A;Note: helps maintain cellular cholesterol homeostasis; plays a role in C;Superfamily: sterol O-acyltransferase C;Keywords: acyltransferase; cholesterol merahalizers.
                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-550 <CHA2>
A; Cross-references: UNIPROT: P35610; UNIPARC: UPI0000135B5D;
R; Chang, C.C.Y.; Huh, H.Y.; Cadigan, K.M.; Chang, T.Y.
J. Biol. Chem. 268, 20747-20755, 1993
A; Title: Molecular cloning and functional expression of hum
A; Reference number: A48026; MUID: 94012607; PMID: 8407899
A; A; Accession: A48026
                                                                                                                                        A;Gene: GDB:SOAT; STAT; ACAT
A;Cross-references: GDB:251696; OMIM:102642
A;Map position: 1q25-1q25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 28-May-1999 #sequence_revision C;Accession: A59038; A48026 R;Chang, C.C.Y; Chang, T.Y. submitted to GenBank, May 1999 A;Description: Molecular cloning and fu
                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-206, R', 208-550 < CHA1 >
A; Crose-references: UNIPARC: UPI000014346C;
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sterol O-acyltransferase (EC 2.3.1.26) - human N;Alternate names: ACAT; acyl-coenzyme A cholesterol acyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYGNAAVWLSLIIGOPIAVLMYVHDYYV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSKW--MARTGVFLASAFFHEYLVSVPLR----MFRLWAFTGMMAQIPLAWFVGRFFQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCLFYVYY---IFERLCAPLFRNIKQEPF8----ARVLVLCVFNSILPGVLILFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QV-------VSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKRFKSAAMLAVFALSAVVHEYALAICLSYFYPVLFVLFMFFGM----AFNFIVNDSRKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --QYLYFLFAPTLIYRDNYPRTPTVRWGYVAMQFLQVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 09-Jul-2004
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cholesterol metabolism; coenzyme A; endoplasmic reticulum; phydrate (Asn) (covalent) #status predicted

the development

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C; Date: 2...
C; Accession: S63350
C; Accession: S63350
R; Pohl, T.M.
submitted to the Protein Sequence Database, ...
A; Reference number: S63346
A; Accession: S63350
A; Accession: S6350
A; Residues: 1-642 <POH>
A; Cross-references: UNIPROT: P53629; UNIPARC: UPI0000125DBD; EMBL: Z71634; NID: g1302503; PI
A; Experimental source: strain S288C
C; Genetics:
A; Experimental source: strain S288C
C; Cenetics:
A; Cross-references: SGD: S0005302; MIPS: YNR019w
A; Map position: 14R
C; Superfamily; probable membrane protein
C; Keywords: transmembrane protein
F; 219-235/Domain: transmembrane #status predicted <TM1>
F; 225-331/Domain: transmembrane #status predicted <TM3>
F; 321-337/Domain: transmembrane #status predicted <TM5>
F; 321-337/Domain: transmembrane #status predicted <TM5>
F; 321-337/Domain: transmembrane #status predicted <TM6>
The company of the com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YNR019w - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein N3206 (;Speciaes: Saccharomyces cerevisiae C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-U-C;Accession: S63350 #sequence_revision 03-May-1996 #text_change 09-U-C;Accession: S63350
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  LTBN---ILKLHWLSKIFLFLHSLVLLMKWHSFAFYNGYLWGIKEELQFSKSALAKYKDS
                                              LTEQAGLLLHVANLATILCFPAAVVLLVE--SITPVGSLLALMAHTILFLK--LFSYRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNGVLLCFYSQEWYARRHCPLKNPTFLDYVRP
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26.8%; Pred. No. 1.4e-20;
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C;Superfamily: probable membrane protein YCR048w
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A;Residues: 1-472 <WED>
A;Cross-references: UNIPROT:Q9UU82; UNIPARC:UPI000069EC3;
A;Experimental source: strain 972h-; clone p1 p1E11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 VNSWCRRARAKAASAGKK------ASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNFPRSPRIRKRFLLRRILEM---LFFTQLQVGLIQQWMVPTIQNSMKPFKDMDYSRIIE
                                           VFLASAFFHEYLVSVPLRMFRLWAFTGMMAQIPLAWFVGRFFQGNY---GNAAVWLSLII 463
                                                                                                                          NAVABLMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMLQMPLVALTNTKFMRNRTIIGNVIFWLGICMGPSVMCTLYL
  TFFVSSVLHELVMGCITLKIRGYGLFFQMTQIPYIIIQRQKFVRRHRLLGNIAFWFSIII
                                                                                                 NFSAEITRFADRNFYDDWWNCWTWDQFARTWNKPVHYFLLRHVYVP-LNSFMSKSLSTFF
                                                                                                                                                                                               ISDHFMVPVLAKAIRTIIEAPEDASATYFAIRLGHTVAFLMFPFMLSFLLVFWVIFEGVC
                                                                                                                                                                                                                                                                                              CLNHHGNTYPENLTIPNALDFLFMPSLCYQLYYPRTAHVRIHYLIECALGTFGCIFLLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                             ITPVGSLLALMAHTILFLKLFSYRDVNSW---CRRARAKAASA-----GKKASSAAAPH
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                                                                                                                                                                                                                                             LIQQWMVPTIQNSMKPFKDM--DYS-----RIIERLLKLAVPNHLIWLIFFYWLFHSCL
                                                                                                                                                                                                                                                                                                                                              TV-----SYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFTQLQVG
                                                                                                                                                                                                                                                                                                                                                                                               WSWTHRAMFILHSMVILMKLHSYNVVNGWYSYCYHSLNKLQSKKTDLDDDERSSVEFYEH
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26.7%;
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A; Molecule type:. DNA
A; Residues: 1-537 <CON>
A; Cross-references: UNIPROT:Q10269; UNIPARC:UPI0000125DC3; EMBL:Z69729; NID:g1204167; R; Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996
A; Reference number: Z21732
A; Accession: T37855
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C;Superfamily: probable membrane protein YCR048w
C;Keywords: acyltransferase; coenzyme A
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S67434
                                                                                                                                                                                                                                                                                                        RESULT 10
T18744
                                                                                                                                                                                                  hypothetical protein B0395.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T18744
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R;Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, February 1996
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submitted to the EMBL Data Library, November 1995
A;Reference number: Z19014
A;Reference number: Z19014
A;Accession: T1874
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-467 <WILD
A;Cross-references: UNIPROT:Q17498; UNIPARC:UPI000007E76B; EMBL:Z68131; PIDN:CAA92217.1;
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A;Molecule type: DNA
A;Residues: 1-537 <CO2>
A;Cross-references: UNIPARC:UPI0000125DC3; EMBL:Z69729; PIDN:CAA93593.1; GSPDB:GN00066;
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A;Cross-references: UNIPROT:P25628; UNIPARC:UPI000003B3AA; EMBL:X59720; NID:g1907116; PI R;Bolotin-Fukuhara, M.; Buhler, J.M.; Daignan-Fornier, B.; Doira, C.; Francingues-Gailla submitted to the Protein Sequence Database, March 1992
A;Reference number: S19396
A;Accession: S19762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Grivell, L.A.; de Haan, M.; Maat, M.J. submitted to the Protein Sequence Database, A;Reference number: S19412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein YCR048w - yeast (Saccharomyces cerevisiae) C;Species: Saccharomyces cerevisiae C;Species: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-J
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                                                                                      F;453-469/Domain:
                                                                                                          F;401-425/Domain:
                                                                                                                        F;370-387/Domain:
                                                                                                                                         F;289-305/Domain:
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C;Superfamily: probable membrane protein YCR048w
                                                                                                                                                                                                                                                              A; Cross-references: SGD: S0000644; MIPS: YCR048w
                                                                                                                                                                                                                                                                                  A; Gene: SGD: ARE1
                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPARC: UPI0000178837; EMBL: X59720; MIPS: YCR048w
                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-328 < BOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-610 <GRI>
Query Match
Best Local Similarity
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10.9%;
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 281.5; DB 2
No. 2.8e-15;
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                                                                                                                                                           ~TM1 > 
~TM2 >
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sterol O-acyltransferase (EC 2.3.1.26) - rabbit (fragment)
N;Alternate names: acyl-coenzyme A cholesterol acyltransferase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I47040
R;Pape, M.E.; Schultz, P.A.; Rea, T.J.; DeMattos, R.B.; Kieft, K.; Bisgaier
J. Lipid Res. 36, 823-838, 1995
A;Title: Tissue specific changes in acyl-CoA: cholesterol acyltransferase (A;Accession: I47040; MUID:95341197; PMID:7616126
A;Accession: I47040
A;Status: preliminary; translated from GB/EMBL/DDBJ
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I47040
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q95214; UNIPARC:UPI000008764A; GB:S78180; NID:g1515471; C;Comment: This enzyme helps maintain cellular cholesterol homeostasis by catalyzing y cholesterol and oxygenated sterols. C;Superfamily: sterol O-acyltransferase C;Superfamily: sterol O-acyltransferase; cholesterol; coenzyme A; endoplasmic reticulum; transme C;Keywords: acyltransferase; cholesterol; coenzyme A; endoplasmic reticulum;
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A; Residues: 1-305 < PAP>
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GLIQQWMVPTIQN-SMKPF 311
                                    ---TVPIP---TVNQYLYFLFAPTLIYRDSYPRTPTVRWGYVAMQFAQVFGCLFYVYY--
                                                                        APHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEM---LFFTQLQV
                                                                                                                GFGPTYIVLAYTLPPASRFIVILEQIRLIMK-----AHSFVRENVPRVLNSAKEKSS--
                                                                                                                                                  CFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWCRRARAKAASAGKKASSAA
                                                                                                                                                                                           VVWTWWTMFLSTLSIPYFLFQHWANGYSKSSHPLMYSLF-----HGLLFMVFQLG-IL
                                                                                                                                                                                                                             QVVSLFLKDPHSWPAPCLVIA--ANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATIL
                                                                                                                                                                                                                                                                     LLDELFEVD----HIRTIYHMFIALLILFILSTLVVDYIDEGRLVLEFNLLSYAFGKLPT
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24.3%;
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                                                                                                                                                                                                                                                                                                                                                                  Score 131.5; DB 2;
Pred. No. 0.0029;
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F;492-508/Domain:
F;529-545/Domain:
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A;Cross-references: UNIPROT:P53154; UNIPARC:UPI000013B0BC; EMBL:Z72606; NID:g1322606; PI
A:Experimental source: strain S288C
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A; Accession: S64091
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A;Cross-references: SGD:S0003052
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                                                                          AFWRAWHRSYNKWVVRYIYIPL---GGSKNRVLTSLAVFSFVAIWHD----IELKLL-LW
                                                                                                                YFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMART--GVFLASAFFHEYLVSVPLRMFRLW
                                                                                                                                                                                                                                                                                                                                                                                          FINDNFRAYPFGNICSFLSPLDHWYRGIIPRWDVFFNFTLLRVLSYNLDFLERWENLQKK 243
                                        AFTGMMAQIP------LAWF-----VGRFFQGNYGNAAVWLSLI 462
                                                                                                                                                         FNLN---II--WLKLLIP----WRLFRLWALLDGIDTPENMIRCVD-----NNYSSL
                                                                                                                                                                                                                                     YQSKHTLPSINFKFIFYYAVRFVIALLSMEFILHFLHVVAISKTKAWENDTPFQISMIGL
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  GWLIVLFLLPEIFATQIFSHYTDAVWYRHVCAVGAVFN-----IWVMMI
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sn-glycerol-3-phosphate permease [imported] - Escherichia coli (strain O157:H7, su
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85863
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.;
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Ap
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85863
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G85863
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C;Superf
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C;Species: Besherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E91019
R;Hayashi, T.; Mekino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H
gasawara, N.; Yabunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91019
A;Molecule type: DNA
A;Residues: 1-452 <STO>
A;Cross-references: UNIPROT:Q8X5A0; UNIPARC:UPI00000D0CED; GB:AE005174; NID:g12516580;
A;Experimental source: strain 0157:H7, substrain EDL933
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A;Experimental sburce: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A; Residues: 1-452 <HAY>
                                                                                                A; Status: preliminary
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C;Superfamily: hexose phosphate transport protein uhpT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.5%; Score 117.5; DB 2; Length 452; Best Local Similarity 18.7%; Pred. No. 0.066; Matches 68; Conservative 52; Mismatches 120; Indels 123
                                       470
                                                                                                                                                                                                            350
337
                                                                                 294 -AYFFYEY------AGIPGTLLCGWMSDKVFRGNRGATGVFFMTLV--TIAT
                                                                                                                          410
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                                                                                                                                                                                                                                                                                               297
                                                                                                                                                                                                                                                                                                                                         171
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                                                                                                                                                                    265 VYLLRYG----ILDW----SPTYLKE-----VKHF-----ALDKSSW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                       LMY 472
                                                                                                         ASAFFHEYLVSVPLRMFRLWAFTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAV 469
IVY 339
                                                                                                                                                                                                                                                                             QQWMVPTIQNSMKPFKDMDYSRIIER------LLKLAVPNHLIWLIFFYWLFHSCLNAV
                                                                                                                                                                                                                                                                                                                                         IPPLLFLLGMAWFNDWHAALYMPAFC----
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                                                                                                                                                                                                                                                                                                                                                                                                                        ----WATSSIAVMFVLLFLCGWFQGMGWPPCGRTMVHWWSQKERGGIVSVWNCAHNVGGG
                                                                                                                                                                                                            AELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFL
                                                                                                                                                                                                                                                 QSCGLPPIEEYKNDYPD-DYNEKAEQELTAKQIFMQYVLPNKLLWYI-----AIANVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Mismatches 120; Indels 123;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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        2594
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seq length: 2000000000
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/Backfiles1.pep:*
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2 US-09-165-042-1
2 US-09-326-203A-17
2 US-09-139-6-203A-17
2 US-09-103-754A-5
2 US-09-103-754A-4
2 US-09-103-754A-4
2 US-09-326-203A-18
2 US-09-593-359-4
2 US-09-593-359-4
2 US-09-774-639-125
2 US-09-774-639-125
2 US-09-165-042-3
3 US-09-326-203A-23
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Sequence 1, Appli
Sequence 17, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 18, Appli
Sequence 2, Appli
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Sequence 230, Appli
Sequence 125, Appli
Sequence 11030, Appli
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361 YRDWWNSESVTYFWONWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVS	301 VPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREF 	241 VSYPDNLTYRDLYYFLFAPTLCYELNFPRBPRIRKRFLLRRILEMLFFTQLQVGLIQQWM 	181 AVVLLVESITÞVGSLLALMAHTILFLKLF6YRDVNSWCRRARAKAASAGKKASSAAAPHT 	121 VSLFLKDÞHSWÞAÞCLVIAANVFAVAAFQÝEKRLAVGALTEQAGLLLHVANLATILCFÞA 	61 SGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDÞIQV 	1 MGDRGSSRRRRTGSRPSSHGGGGPAAAEEÉVRDAAAGPDVGAAGDAPAPAPNKDGDAGVG 	ry Match 100.0%; Score 2594; DB 2; Length 488; t Local Similarity 100.0%; Pred. No. 1.6e-255; ches 488; Conservative 0; Mismatches 0; Indels 0; Gaps	ALIGNMENTS ESULT 1 S-09-165-042-1 S-09-165-042-2 Patent No. 6100077 GENERAL INFORMATION: APPLICANT: Sturley, Stephen L. APPLICANT: Oelkers, Peter TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL TITLE OF INVENTION: ACYLTRANSFERASE FILE REFERENCE: 0575/56331 CURRENT APPLICATION NUMBER: US/09/165,042 CURRENT APPLICATION NUMBER: US/09/165,042 SCOTTWARE: Patentin Ver: 2.0 SEQ ID NO 1 LENGTH: 488 TYPE: PRT ORGANISM: Yeast S-09-165-042-1	8 255 9.8 47 2 US-09-774-639-239 Sequence 239, Appli 145 5.6 53 2 US-09-165-042-8 Sequence 8, Appli 117 5.3 52 US-09-165-042-6 Sequence 6, Appli 118 5.2 26 2 US-09-165-042-6 Sequence 235, Appli 2134 5.2 26 2 US-09-774-639-235 Sequence 235, Appli 2132 5.1 52 2 US-09-774-639-235 Sequence 236, Appli 2134 3.3 20 2 US-09-165-042-17 Sequence 216, Appli 217 4.3 250 2 US-09-165-042-17 Sequence 217, Appli 218 4.3 250 2 US-09-165-042-17 Sequence 217, Appli 219 4.3 250 2 US-09-165-042-17 Sequence 218, Appli 219 4.3 250 2 US-09-248-796A-14863 Sequence 10, Appli 219 4.3 2 US-09-489-039A-8293 Sequence 10, Appli 103.5 4.1 33 2 US-09-489-039A-8293 Sequence 2056, Appli 101.5 3.9 432 2 US-09-495-39A-9368 Sequence 2, Appli 3101.5 3.9 432 2 US-09-255-368-2 Sequence 2, Appli 3101.5 3.9 432 2 US-09-358-036-2 Sequence 2, Appli 3101.5 3.9 432 2 US-09-538-036-2 Sequence 2, Appli 3101.5 3.9 432 2 US-09-538-036-2 Sequence 2, Appli 3101.5 3.9 437 2 US-09-790-838-2
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APPLICANT: Ruezinsky, Diane
APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucl
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucl
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucl
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT APPLICATION NUMBER: 60/088,143
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR APPLICATION NUMBER: 60/18,389
PRIOR APPLICATION NUMBER: 60/18,389
PRIOR PILLNG DATE: 1998-11-12
NUMBER: OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 500
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US-09-326-203A-17
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 427;
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ORGANISM: Rattus
-09-326-203A-17
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                                               FLASAFFHEYLVSIPLRMFRLMAFTAMYAQVPLAWIVNRFFQGNYGNAAVWVTLIIGQPV
                                                                                                                                                                         FTQLQVGLIQQWMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLN
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Pred. No. 1.8e-225;
6; Mismatches 31;
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US-09-103-754A-5
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US-09-899-645A-8
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Sequence 5, Application US/09103754A PATENT NO. 6344548
GENERAL INFORMATION:
APPLICANT: Farese, Robert
APPLICANT: Cases, Sylvaine
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SEQ ID NO 8
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APPLICANT: Zheng, Peizhong
APPLICANT: Nichols, Scott
TITLE OF INVENTION: WETHODS FOR REGULATING BETA-OXIDATION IN
FILE REFERENCE: 35718/235742
CURRENT APPLICATION NUMBER: US/09/899,645A
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/216,211
PRIOR PILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 498
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 87.8%; Score 2278.5; DB 2; Local Similarity 85.1%; Pred. No. 2.4e-223; 1es 421; Conservative 29; Mismatches 34;
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Best Local S
Matches 420
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
OPERATING SYSTEM: DOS
SOFTWARE: FREESEQ for
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TITLE OF INVENTION: Diacylgl
TITLE OF INVENTION: sferase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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TELEPHONE: 650 327 3400
TELEFAX: 650 327 3231
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NAME: Field, Bret E
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 65
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/103,754A
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Similarity 84.8%; Pred. No. 7.8e-223;
20; Conservative 29; Mismatches 35;
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                ABLMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFL
                                                                                QLQVGLIQQWMVPTIQNSMKPFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAV
                                                                                                                                               KKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFT
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AELLQFGDREFYRDWWNAESVTYFWQNWNIPVHKWCIRHFYKPMLRHGSSKWVARTGVFL
                                                                                                                        KKVSGAAAQQAVSYPDNLTYRDLYYFIFAPTLCYELNFPRSPRIRKRFLLRRVLEMLFFT
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                                                                                                                                                                                          Matches 384;
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Best Local :
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NAME: Field, Bret E
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SOFTMARE: FASESEG FOR Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,754A
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
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APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatik
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TITLE OF INVENTION: Diacylglycerol O-acyltran
TITLE OF INVENTION: sferase
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ADDRESSEE: Bozicevic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 37,620 REFERENCE/DOCKET NUMBER: 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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                     AKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRI
                                                                             AGLLHVANLATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWCRRAR
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                                                                                                                          LFLENLIKYGILVDPIQVVSLFLKDPYSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQ
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 <u>AKAASAGKKASSVAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRI</u>
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Cases, Sylvaine
Smith, Steven
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                                                                                                                                                                                          Conservative
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linear
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                                                                                                                                                                                                         78.6%;
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                                                                                                                                                                                        Score 2039; DB 2;
Pred. No. 4.3e-199;
L; Mismatches 1;
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                                                                                                                                                                                                                     Length 386;
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; LENGTH: 496
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-326-203A-18
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US-09-326-203A-18
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GENERAL INFORMATION:
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APPLICANT: Ruszinsky, Diane
APPLICANT: Ruszinsky, Diane
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
TITLE OF INVENTION: Acid Sequences
TILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEC ID NOS: 46
SCRUTWARER: Patentin Ver: 2.1
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                 CLNAVAELMQFGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWWAR
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FLNLIAELLRFADREFYRDFWNAETIGYFWKSWNIPVHRFAVRHIYSPMMRNNFSKMSAF
                                                                                                                                            KQFWDLKDELSMHQMAAQYPANLTLSNIYYFMAAPTLCYEFKFPRLLRIRKHFLIKRTVE
                                                                                                                                                                               -----APHTVS--YPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILE
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-326-203A-2
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Best Local Similarity
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/326,203A CURRENT FILING DATE: 199-06-04 PRIOR APPLICATION NUMBER: 60/088,143 PRIOR FILING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60/108,389 PRIOR FILING DATE: 1998-11-12 NUMBER: 0F SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                                                                                                  QKYISEPVVIFIHIIIMTEVLYPVYVTLACDSAFLSGVTLMLLT-CIVWLKLVSYAHTS
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                                                                                                    KPMLRRGSSKWMARTGVFLASAFFHEYLVSVPLRMFRLWAFTGMMAQIPLAWFVGRFFQG
                                                                                                                                            LYVWLCMFYCFFHLWLNILAELLCFGDREFYKDWWNAKSVGDYWRMWNMPVHKWMVRHIY
                                                                                                                                                               HLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSESVTYFWQNWNIFVHKWCIRHFY 390
                                                                                                                                                                                                                 CIRKGWVARQFAKLVIFTGFMGFIIEQYINPIVRNSKHPLKGDLLYA--IERVLKLSVPN
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Ruezinsky, Diane
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 REGSTVGNMIFWEIECIEGOPMCVLLYYHD
                                  NY----GNAAVW-LSLIIGQPIAVLMYVHD 475
                                                                      FPCLRSKIPKTLAIIIAFLVSAVFHELCIAVPCRLFKLWAFLGIMFQVPLV-FITNYLQB
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Pred. No. 9.5e-72;
77; Mismatches 174;
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GENERAL INFORMATION:

APPLICANT: LAroche, Andre J.

APPLICANT: Wykiforuk, Cory L.

APPLICANT: Weselake, Randall J.

TITLE OF INVENTION: Diacylglycerol O-acyltransferase

FILE REFERENCE: 24015US0

CURRENT APPLICATION UNUBER: US/09/593,359

CURRENT FILING DATE: 2000-06-14

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 503

TYPE: PRT
ORGANISM: Brássica napus

OTHER INFORMÁTION: DGAT1

US-09-593-359-4
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US-09-593-359-4
                                                                                  Sequence 2, Application US/09593359 Patent No. 6552250 GENERAL INFORMATION:
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Best Local Similarity
Matches 191; Conserv
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APPLICANT: Laroche, Andre J.
APPLICANT: Nykiforuk, Cory L.
APPLICANT: Westlake, Randall J.
TITLE OF INVENTION: Diacylglycerol O-acyltransferase
FILE REFERENCE: 24015US0
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; Patent NO. WOLLER
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; TITLE OF INVENTION: 90 Human Secreted Proteins
; TITLE OF INVENTION: 90 Human Secreted Proteins
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; NUMBER OF SEQ ID NOS: 371
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                                                                                                                                                                                                                                ; ORGANISM: Homo US-09-774-639-230
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US-09-774-639-230
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; ORGANISM: Brassica
; OTHER INFORMATION:
US-09-593-359-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/593,359
CURRENT FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 341
                                                                                                                                                     Query Match
Best Local Similarity
Matches 105; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 230, Application Patent No. 6806351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                           LENGTH: 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 25.3%;
Local Similarity 41.9%;
                                    431
                                                                                                 377 WNIPVH-----KWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVSVPLRMFRLWA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                    FTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLNYEAPAAEA 488
                                                                          WINMAVNILNRFPCPLLCRHFYKPMLRRGSSKWMARTGVFLASAFFHBYLVSVPLRMFRIWA 105
FTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLNYBAPAAEA 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVPLV-FITNFLQERFGSMVGNMIFGSASCIFGQPMCGLLYYHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIPLAWFVGRFFQGNYGNAAVWL----SLIIGQPIAVLMYVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WNMPVHKWMVRHVYFPCLRIKIPKVPAIIIAFLVSAVFHELCIAVPCRLFNLWAFMGIMF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVSVPLRMFRLWAFTGMMA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A--IERVLKLSVPNLYVWLCMFYCFFHLWLNILAELLCFGDREFYKDWWNAKSVGDYWRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMOFGDREFYRDWWNSESVTYFWON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APTICYELNEPRSPRIRKRELLRRILEMLEFTQLQVGLIQQWMVPTIQNSMKPEK-DMDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLT-CIVWLKLVSYAHTNYDIR----TLANSSDKANP----EVSY--YVSLKSLAYFML
                                                                                                                                                       Conservative
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                                                                                                                                                                    21.2%;
89.0%;
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                                                                                                                                                   Score 551; DB 2; 1
Pred. No. 5.7e-48;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 656.5; DB 2; Pred. No. 3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 117;
                                                                                                                                                                                        Length 163;
                                                                                                                                                       Indels
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GENERAL INFORMATION:

APPLICANT: Sturley, Stephen L.

APPLICANT: Scurley, Peter

ITITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL

ITITLE OF INVENTION: ACYLTRANSFERASE

FILE REFERENCH: 0575/56331

CURRENT APPLICATION NUMBER: US/09/165,042

CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3

LENGTH: 522

TYPE: PRT

ORGANIGM: Yeast
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; LOCATION: (75)
; OTHER INFORMATION: Xaa equals stop translation
US-09-774-639-125
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US-09-165-042-3
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US-09-774-639-125
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TITLE OF INVENTION: 90 Human Secreted Proteins

FILE REFERENCE: PZ013P1

CURRENT APPLICATION NUMBER: US/09/774,639

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/244,112

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 371

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 125

LENGTH: 75

TYPE: DET
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 127; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09165042 Patent No. 6100077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 MDYSRIIERLIKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSESVTYF 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 WQNWNIPVHKWCIR 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74;
                                                                                   135 IISTLAIDFIDEGRLLLEFDLLIFSFGQLPLALVTWVPMFLST
                                                                                                                                                                                                                                                       127; Conservative
                                                                                                                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                         45 DAPAPAP-----NKDGDAGVGSGHWELRCHRLQDSLFSSDSGFSNYRGILNW-----CVV 94
                                     VAAFQVEKRLAVGALTEQAGL-LLHVANLATILCFPAAVVLLVESITPVGSLLALMAHTI 203
                                                                                                             ML-----ILSNARLFLE-NLIKYGILVDPIQVVS---LFLKDPHSWPAPCLVIAANVFA 144
  LAPYQALRIWARGTWTQATGLGCALLAAHAVVLC-ALPVHVAVEHQLPPASRCVLVFEQV
                                                                                                                                                                    DKPLPPPPPGSLSRTQEPSLG----KQKVFIIRKSLLDELMEVQHFRTIYHMFIAGLCVF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSESVTYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%; Score 431; DB 2; lilarity 100.0%; Pred. No. 3.1e-36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                 14.5%; Score 375.5; DB 2; 26.3%; Pred. No. 2.4e-29; tive 75; Mismatches 189;
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                                                                                                                                                                                                                                                                                             Length 522;
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    237
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US-09-949-016-11030
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11030
LENGTH: 522
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398
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                                      262 CYELNFPRSPRIRKRFLLRRILEMLFFTQLQVGLIQQWMVPTIQN-SMKPFKDMDYSRII 320
                                                                                                                                204 LFL-KLFSY-RDVNSWCRRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTL 261
                                                                                                                                                                                                                         145 VAAFQVEKRLAVGALTEQAGL-LLHVANLATILCFPAAVVLLVESITPVGSLLALMAHTI 203
                                                                                                                                                                                                                                                                         135 IISTLAIDFIDEGRLILEFDLLIFSFGQLPLALVTWVPMFLST-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 MMAQIPL-----AMFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLNYEAPAA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 LSILHATLPGIFMLLLIFFAFLHCWLNAFAEMLRFGDRMFYRDWWNSTSFSNYYRTWNVV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 LFL-KLFSY-RDVNSWCRRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTL 261
                                                                                                                                                                                                                                                                                                               95 ML-----ILSNARLFLE-NLIKYGILVDPIQVVS---LFLKDPHSWPAPCLVIAANVFA 144
                                                                                                                                                                                                                                                                                                                                                                   79
                                                                                                                                                                                                                                                                                                                                                                                                          45 DAPAPAP-----NKDGDAGVGSGHWELRCHRLQDSLFSSDSGFSNYRGILNW-----CVV 94
                                                                                                                                                                           LAPYOALRIMARGTWTQATGLGCALLAAHÁVVLC-ALPVHVAVEHQLPPASRCVLVFEQV 237
                                                                                 RFLMKSYSFLREAVPGTLRAR------RGEGIQAPSFSSY------LYFLFCPTL
                                                                                                                                                                                                                                                                                                                                                                   DKPLPPPPPGSLSRTQEPSLG----KQKVPIIRKSLLDELMEVQHFRTIYHMFIAGLCVF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFLMKSYSFLREAVPGTLRAR-----RGEGIQAPSFSSY------LYFLFCPTL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHKWCIRHFYKPMLR--RGSSKWMARTGVFLASAFFHEYLVSVPLRMFR-----LWAFTG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSESVTYFWQNWNIP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYRETYPRTPYVRWNYVAKNFAQALGCVLYACFILGRLCVPVFANMSREPFST---RALV 337
IYRETYPRTPYVRWNYVAKNFAQALGCVLYACFILGRLCVPVFANMSREPFST---RALV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHDWLYSYVYQDGLRLLGARARGVAMLGVFLVSAVAHEYIFCFVLGFFYPVMLILFLVIG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09949016
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 375.5; DB 2; 26.3%; Pred. No. 2.4e-29; tive 75; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVLMWTMLFLGQGIQVSLYCQEWYARRH-CPLP 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 522;
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RESULT 14
US-09-326-203A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 409
TYPE: PRT
ORGANISM: murine
PUBLICATION INFORMATION:
JOURNAL: J. Biol. Chem.
VOLUME: 270
PAGES: 26192-26201
DATE: 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/326,203A CURRENT FILING DATE: 1999-06-04 PRIOR APPLICATION NUMBER: 60/088,143 PRIOR FILING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60/108,389 PRIOR FILING DATE: 1998-11-12 NUMBER: 05 EQ. ID NOS: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Acyl-COA:Cholesterol Acyltransferase Related Nucleic
TITLE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                         338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 VHKWCIRHFYKPMLR---RGSSKWMARTGVFLASAFFHEYLVSVPLRMFR-----LWAFTG
                                                                                                                                                                                                                                                                                     167 LHVANLATIICFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWCRRARAKAA
                                                                                                                                                                                                                                                                                                                                                                            119 QV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23, Application US/09326203A
). 6444876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 MMAQIPL-----AWFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLNYEAPAA 486
                                                                                                                                                                                                                                                                                                                                   60 VIWTWWAMFLSTLSIPYFLFQP--W-----AHGYSKSSHPLIYSLV------HGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 LQDSLFSSDSGFSNYRGILNWCVVMLIL-----SNARLFLE-NLIKYGILVDPI 118
                                                                                                                                                                                                                                            FLVFQLG-VLGFVPTYVVLAYTLPPASRFILILEQIRLIMK-----AHSFVRENIPRVL
                                                                                                                                                      NAAKEKSSKOPLPTVN-----QYLYFLFAPTLIYRDNYPRTPTVRWGYVAMQFLQVF
                                                                                                                                                                                                 SAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWMNSESVTYFWQNWNIP
FYMLFHSCLNAVAELMQFGDREFYRDWWNSESVTYFWQNWNIFVHKWCIRHFYKPMLRRG
                                                                    GCLFYVYY---IFERLCAPLFRNIKQEPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Ver. 2.1
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                                                                                                          --LFFTQLQVGLIQQWMVPTIQN-SMKPFKDMDYSRIIERLLKLAV-----PNHLIWLIF
                                                                                                                                                                                                                                                                                                                                                                                                                    LLDELFEVD----HIRTIYHMFIALLILFVLSTIVVDYIDEGRLVLEFNLLAYAFGKFPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHDWLYSYVYQDGLRLLGARARGVAMLGVFLVSAVAHBYIFCFVLGFFYPVMLILFLVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lassner, Mike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.3%; Score 370.5; DB 2
27.5%; Pred. No. 5.5e-29;
                                                                                                                                                                                                                                                                                                                                                                         --VSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NVLMWTMLFLGQGIQVSLYCQEWYARRH-CPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                    ---ARVLVLCVFNSILPGVLILFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
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US-09-328-857A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application Patent No. 6579974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 502
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 6510-104US1
CURRENT APPLICATION NUMBER: US/09/328,857A
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/090,354
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Farese, Robert
APPLICANT: No. 6579974Ak, Sabine
APPLICANT: Brickson, Sandra
TITLE OF INVENTION: No. 6579974el Acyl CoA:Cholesterol Acyl
TITLE OF INVENTION: Transferase (ACAT-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: UNSURE LOCATION: (191)...
                           441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 SNARLFLE---NLIKYGILVDPIQVVS---LFLKDPHSWPAPCLVIAANVFAVAAFQVEK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 DAPAPAPNKDGDAGVGSGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVML-----IL 98
                                                                    YVYQDGLRLLGARARGVAMLGVFLVSAVAHEYIFCFVLGFFYPVMLILFLVIGGMLNFMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLAVGALTEQAGL--LLHVANLATILCFPAAVVLLVESITPVGSLLALMAHTILFL-KLF
  -----AMFVGRFFQGNYGNAAVMLSLIIGQPIAVLMYVHDYXVLNYEAPAAEA 488
                                                                                                          HFYKPMLR---RGSSKWMARTGVFLASAFFHEYLVSVPLRMFR----LWAFTGMMAQIPL
                                                                                                                                                                                            VPNHLIWLI FFYWLFHSCLNAVABLMQFGDREFYRDWWNSESVTYFWQNWNI PVHKWCIR
                                                                                                                                                                                                                                            RTPYVRWNYVAKNFAQALGCVLYACFILGRLCVPVFANMSRDPFST---RALVLSILHAT 324
                                                                                                                                                                                                                                                                                       RSPRIRKRFLLRRILEMLFFTQLQVGLIQQWMVPTIQN-SMKPFKDMDYSRIIERLLKLA
                                                                                                                                                                                                                                                                                                                                                                            SY-RDVNSWCRRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFP
                                                                                                                                                                                                                                                                                                                                                                                                                    LWARGTWTQATGLGCALLAAHAVVXCALPVHVA--VEHQLPPASRCVLVFEQVRFLMKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEGRILLEFDPLIFSFGQL--PLALVTWVPMFLST-------LLAPYQALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKPLPPP---PPGSLSSELMEVQHFRTIYHMF-----IAGLCVFIISTLAIDFI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIWNIMVWASLFLGYGLILCFYSQEWY 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYGNAAVWLSLIIGOPIAVLMYVHDYY 477
                                                                                                                                                      LPGIFMLLLIFFAFLHCWLNAFAEMLRFGDRMFYRDWWNSTSFSNYYRTWNVVVHDWLYS
                                                                                                                                                                                                                                                                                                                              SFLREAVPGTLRAR-----RGEGIQAPSFSSY------LYFLFCPTLIYRETYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cases, Sylvaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKRFKSAAMLAVFALSAVVHEYALAICLSYFYPVLFVLFMFFGM----AFNFIVNDSRKR 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSKW--MARTGVFLASAFFHEYLVSVPLR----MFRLWAFTGMMAQIPLAWFVGRFFQG 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFAFLHCWLNAFAEMLRFGDRMFYKDWWNSTSYSNYYRTWNVVVHDWLYYYVYKDLLWFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Xaa is any
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 367.5; DB 2;
Pred. No. 1.5e-28;
4; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                  2594
2278.5
791.5
779.5
779
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551
431
375.5
259
259
255
118
114.5
101.5
1001.5
1001.5
1001.5
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                                                                                                                                                                                                                                                                                                                       Score
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1: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep:*

2: /SIDSS/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /SIDSS/ptodata/1/pubpaa/US07 NEW PUB.pep:*

4: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep:*

5: /SIDSS/ptodata/1/pubpaa/US08 NEW PUB.pep:*

6: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep:*

7: /SIDSS/ptodata/1/pubpaa/US09 NEW PUB.pep:*

8: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:*

9: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:*

10: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:*

11: /SIDSS/ptodata/1/pubpaa/US11 NEW PUB.pep:*

12: /SIDSS/ptodata/1/pubpaa/US10 NEW PUB.pep:*
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length: 2000000000
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Gapop 10.0 , Gapext 0.5
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2594
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MGDRGSSRRRRTGSRPSSHG.....VLMYVHDYYVLNYEAPAAEA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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4488
5503
3447
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10 US-10-986-501-306
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10 US-10-986-501-307
10 US-10-986-501-308
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         Sequence 5, Appli
Sequence 4, Appli
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Sequence 9, Appli
Sequence 8, Appli
Sequence 155, Appli
Sequence 1030, Appli
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Sequence 306, Appli
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•	Sequence 37, Appl	Sequence 35, Appl	Sequence 4, Appli	Sequence 9, Appli	Sequence 13811, A	Sequence 5, Appli	Sequence 9682, Ap	Sequence 304, App	Sequence 306, App	Sequence 10876, A	Sequence 77, Appl	Sequence 20291, A	Sequence 749, App	Sequence 873, App	Sequence 321, App	Sequence 3794, Ap	Sequence 5270, Ap	Sequence 263, App	Sequence 8361, Ap				

ALIGNMENTS

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APPLICANT: Zou, Jitao
APPLICANT: Taylor, David C
APPLICANT: Taylor, David C
APPLICANT: Taylor, David C
APPLICANT: Jako, Colette C
TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
FILE REFERENCE: 3015-5684.1US
CURRENT APPLICATION NUMBER: US/11/317,983
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/11/117,005
PRIOR FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/11/17,005
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR APPLICATION NUMBER: 00/623,514
PRIOR APPLICATION NUMBER: PCT/CA99/01202
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-17
NUMBER: 05 SEO ID NOS: 26
COFFMANDE: DATE: 1998-12-17
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US-11-317-983-5
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Best Local Similarity
Matches 488; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 488
TYPE: PRT
ORGANISM: human
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VSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILCFPA 180
                                                                                                                             SGHWBLRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDPIQV
                                                                                                    SCHWELRCHRLODSLESSDSGESNYRGILNWCVVMLILSNARLELENLIKYGILVDPIQV
                                                                                                                                                                                                     MGDRGSSRRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAPNKDGDAGVG
                                                                                                                                                                                                                                                                                               100.0%; Score 2594; DB 10; Length 488; ilarity 100.0%; Pred. No. 5.2e-224; Conservative 0; Mismatches 0; Indels 0;
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APPLICANT: Zou, Jitao
APPLICANT: Wei, Yangdou
APPLICANT: Wei, Yangdou
APPLICANT: Jako, Colette C
TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
FILE REFERENCE: 3015-5884.US
CURRENT APPLICATION NUMBER: US/11/317,983
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/11/117,005
PRIOR FILING DATE: 2005-04-28
PRIOR FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: WS/123,514
PRIOR APPLICATION NUMBER: WS/123,514
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: FCT/CA99/01202
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1998-12-17
UNMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 498
; TYPE: PRT
; ORGANISM: mouse
US-11-317-983-4
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SEQ ID NO 4
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                                                                                                                                                                                                                                                                                          Query Match 87.8%; Score 2278.5; DB 10; Length Best Local Similarity 85.1%; Pred. No. 8.8e-196; Matches 421; Conservative 29; Mismatches 34; Indels
                                                                              112 GILVDPIQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVAN
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172 LATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWC--RRARAKAASAG
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                                                          GILVDPIQVVSLFLKDPYSWPAPCVIIASNIFVVAAFQIEKRLAVGALTEQMGLLLHVVN
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                                                                                                                                         DKDGRTSVGDGYWDLRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKY
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APPLICANT: Taylor, David C
APPLICANT: Wei, Yangdou
APPLICANT: Wei, Yangdou
APPLICANT: Wei, Yangdou
APPLICANT: Jako, Colette C
TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gen
FILE REFERENCB: 3015-5684.1US
CURRENT APPLICATION UNMBER: US/11/317,983
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/11/117,005
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/112,812
PRIOR APPLICATION NUMBER: 60/112,812
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIN Ver. 2.1
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US-11-317-983-2
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                                                                                                                                                                                                                                                                                                                                                     Query Match 30.5%; Score 791.5; DB 10; Length 520; Best Local Similarity 38.0%; Pred. No. 8.7e-63; Matches 194; Conservative 77; Mismatches 174; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 520
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                                                                                                                                                                                             84 GGDNNGGGRGGGEGRGNADATFTYRPSVPAHRRARESPLSSDAIFKQSHAGLFNLCVVVL
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                                                                        VGALTEQAGLILHVANLATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYR---
                                                                                                                                               ILSNARLFLENLIKYGILV-DPIQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLA 155
                                        OKYISEPVVIFLHIIITMTEVLYPVYVTLRCDSAFLSGVTLMLLT-CIVWLKLVSYAHTS
                                                                                                                                                                                                                                                                                                                  RRRRTGSRPSSHGG------GGPAAAEEE----VRDAAAGPDVGAAGDAPA 48
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  -DVNSWCRRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSP
                                                                                                                                                                                                                                                                            RLRRRKSRSDSSNGLLLSGSDNNSPSDDVGAPADVRDRIDSVVNDDAQG-TANLAGDNNG
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; LENGTH: 503
; TYPE: PRT
; ORGANISM: Brassica napus
US-11-317-983-9
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US-11-317-983-9
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CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/11/117,005
PRIOR FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR PILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 07/CA99/01202
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/112,812
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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                                    229 GKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFF 288
                                                                                                                 169 VANLATILCFPAAVVLLVESITPVGSLLALMAHTILFLKLFSYRDVNSWCRRARAKAASA 228
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DK-----VDPEISY--YVSLKSLAYFMVAPTLCYQPSYPRSPCIRKGWVARQLAKLVIF
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                                                                                                                                                       KYGWLIRTDFWFSSTSLRD---WPLFMCCLSLSVFPLAAFTVEKMVLQKFISEPVAIILH
                                                                                                                                                                                         KYGILV-DPIQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLH
                                                                                                                                                                                                                                  -----DVRFTYRPSVPAHRRTRESPLSSDAIFKQSHAGLFNLCVVVLVAVNSRLIIENLM
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                                                                                                                                                                                                                                                                                                                                                                                     30.1%; Score 779.5; DB 10; 38.7%; Pred. No. 9.8e-62; tive 83; Mismatches 168;
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APPLICANT: Taylor, David C
APPLICANT: Wei, Yangdou
APPLICANT: Wei, Yangdou
APPLICANT: Wei, Yangdou
APPLICANT: Jako Colette C
TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
FILE REFERENCE: 3015-5684.1US
CURRENT APPLICATION NUMBER: US/11/317,983
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/11/117,005
PRIOR APPLICATION NUMBER: US/11/117,005
PRIOR FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: 60/112,812
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US-11-317-983-25
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NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
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APPLICANT: Zou, Jit
APPLICANT: Taylor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 30.0%; Score 778; DB 10; Local Similarity 36.1%; Pred. No. 1.5e-61; les 194; Conservative 77; Mismatches 174;
306
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                    AFLSGVTLMLLT-CIVMLKLVSYAHTSYDIRS-----LANAADKANP----EVSY-
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                                                                                                    ITPVGSLLALMAHTILFLKLFSYR----DVNSWCRRARAKAASAGKKASSAAAPHTVSYP
                                                                                                                                                          --WPLFMCCISLSIFPLAAFTVEKLVLQKYISEPVVIFLHIIITMTEVLYPVYVTLRCDS
                                                                                                                                                                                                                                                             -----SNYRGILNWCVVMLILSNARLFLENLIKYGILV-DPIQVVSLFLKDP 128
                                                                                                                                                                                                                                                                                                                     GGDNNGGGRGGGEGRGNADATFTYRPSVPAHRRARESPLSSDAIFKQSHAGLFNLCVVVL 143
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US-11-317-983-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.3%; Score 656.5; DB 10; Best Local Similarity 41.9%; Pred. No. 6e-51;
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APPLICANT: Taylor, Da
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TYPE: PRT
ORGANISM: Brassica napus
                                                                                              230
                                                                                                                                                                                         172 A--IERVLKLSVPNLYVWLCMFYCFFHLWLNILAELLCFGDREFYKDWWNAKSVGDYWRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144; Conservative
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290
                                           437 QIPLAWFVGRFFQGNYGNAAVWL----SLIIGQPIAVLMYVHD 475
                                                                                                                                            377 WNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVSVPLRMFRLWAFTGMMA 436
                                                                                                                                                                                                                                                                                          112 APTLCYQPSYPRSPCIRKGWVARQFAKLVIFTGLMGFIIEQYINPIVRNSKHPLKGDLLY 171
                                                                                                                                                                                                                                                                                                                                           258
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                                                                                                                                                                                                                                                                                                                                                                                                                                         198 LMAHTILFLKLFSYRDVNSWCRRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLF 257
                                                                                                                                                                                                                                                                                                                                                                                         64 LLT-CIVWLKLVSYAHTNYDIR----TLANSSDKANP-----EVSY--YVSLKSLAYFML
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                                                                                                                                                                                                                                     SRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSESVTYFWQN 376
                                                                                                                                                                                                                                                                                                                         APTLCYELNFPRSPRIRKRFLLRRILEMLFFTQLQVGLIQQWMVPTIQNSMKPFK-DMDY
QVPLV-FITNFLQERFGSMVGNMIFGSASCIFGQPMCGLLYYHD
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                                                                                              WIMPVHKWMVRHVYFPCLRIKIPKVPAIIIAFLVSAVFHELCIAVPCRLFNLWAFMGIMF
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Jako, Colette C
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RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 155, Applic Publication No. US20 GENERAL INFORMATION:
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LENGTH: 163
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Publication No. US20050244845A1
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                                                                PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: 09/244,112
                                                                                                                                                                                                                    FILE REFERENCE: PZ013P2C1
CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2003-07-18
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PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
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CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruben et al.
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PRIOR APPLICATION NUMBER: 60/056,371
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PRIOR FILING DATE: 2001-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US98/16235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                  FILING DATE: 1999-02-04
APPLICATION NUMBER: PCT/US98/16235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431 FTGMMAQIPLAWFVGRFFQGNYGNAAVWL9LIIGQPIAVLMYVHDYYVLNYEAPAAEA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 WNIPVH-----KWCIRHFYKEMLRRGSSKWMARTGVFLASAFFHEYLVSVPLRMFRLWA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 WWMAVNLNRFPCPLLCRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVSVPLRMFRLWA 105
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o. US20050244845A1
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1998-08-04
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Pred. No. 6.5e-42;
2; Mismatches 5;
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HAPPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
ITILE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
ITILE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ.ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ.ID NO 1030
LENGTH: Enc.
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US-10-995-561-1030
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PRIOR FILING BATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING BATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING BATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING BATE: 1997-08-19
PRIOR FILING BATE: 1997-08-19
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LENGTH: 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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281
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                                                                                                                                                                                          145 VAĀFQVEKRLAVGALTEQAGL-LLHVANLATILCFPAAVVLLVESITPVGSLLALMAHTI 203
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                                                                                                                                                                                                                                                      135 IISTLAIDFIDEGRLLLEFDLLIFSFGOLPLALVTWVPMFLST--
                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                              45 DAPAPAP-----NKDGDAGVGSGHWELRCHRLQDSLFSSDSGFSNYRGILNW-----CVV 94
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IYRETYPRTPYVRWNYVAKNFAQALGCVLYACFILGRLCVPVFANMSREPFST---RALV 337
                                     CYELNEPRSPRIRKRELLRRILEMLFETQLQVGLIQQWMVPTIQN-SMKPFKDMDYSRII 320
                                                                               RFLMKSYSFLREAVPGTLRAR------RGEGIQAPSFSSY------LYFLFCPTL 280
                                                                                                                        LFL-KLFSY-RDVNSWCRRARAKAASAGKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTL 261
                                                                                                                                                                  LAPYQALRLWARGTWTQATGLGCALLAAHAVVLC-ALPVHVAVEHQLPPASRCVLVFEQV 237
                                                                                                                                                                                                                                                                                         ML-----ILSNARLFLE-NLIKYGILVDPIQVVS---LFLKDPHSWPAPCLVIAANVFA 144
                                                                                                                                                                                                                                                                                                                                     DKPLPPPPPGSLSRTQEPSLG----KQKVFIIRKSLLDELMEVQHFRTIYHMFIAGLCVF 134
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Pred. No. 1.3e-31;
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PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
                                                                                                                                                                                                                                             Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 305, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                    Query Match
Best Local
                                                                                Matches
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CURRENT FILING DATE: 2004-11-12
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TITLE OF INVENTION: 90 H
FILE REFERENCE: PZ013P2C
                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-08-19
                                                                                                                                                                                LENGTH: 60
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/056,366
FILING DATE: 1997-08-19
APPLICATION NUMBER: 60/056,364
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-08-19
                                       310 PFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSES
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                                                                              60;
PFKDMDYSRIIERLLKLAVPNHLIWLIFFYWLFHSCLNAVAELMQFGDREFYRDWWNSES
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o. US20050244845A1
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                                                                                Conservative
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                                                                                                  100.0%;
                                                                                                                         13.0%;
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                                                                                                  Score 337; DB 9;
Pred. No. 2.5e-23;
                                                                                Mismatches
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                                                                                                                     Length 60
                                                                                Indels
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RESULT 11 US-10-986-501-306

Sequence 306, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
ATTLE OF INVENTION: 90 Human Secreted Proteins

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US-10-986-501-306
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                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 373 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR FILING DATE: 2001-02-01
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PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
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CURRENT FILING DATE: 2004-11-12
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CURRENT FILING DATE: 2004-11-12
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Local Similarity 100.0%;
                                                                                                                                                                                                 FILING DATE: 2000-10-06
APPLICATION NUMBER: 09/244,112
FILING DATE: 1999-02-04
APPLICATION NUMBER: PCT/US98/16235
FILING DATE: 1998-08-04
APPLICATION NUMBER: 60/056,371
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FILING DATE: 1997-08-19
APPLICATION NUMBER: 60/056,364
FILING DATE: 1997-08-19
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FILING DATE: 2000-10-06
APPLICATION NUMBER: 09/244,112
FILING DATE: 1999-02-04
                                                                                                                                FILING DATE: 1997-08-19
APPLICATION NUMBER: 60/056,732
FILING DATE: 1997-08-19
                                             FILING DATE: 1997-08-19
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                                                                                         FILING DATE: 1997-08-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                        Prior
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5. US20050244845A1
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Application data removed - NOS: 373
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; Pred. No. 1.8e-16;
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                   See File Wrapper or PALM
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US-10-986-501-304

Sequence 304, Application US/10986501
Publication No. US20050244845A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PZ013PZC1
CURRENT APPLICATION NUMBER: US/10/986,501

RESULT 14

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US-10-986-501-307
                                                                      Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                             Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 373
SOFTWARE: patentIn Ver. 2.0
SEQ ID NO 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Ruben et al
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Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/986,501
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
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PRIOR FILING DATE: 1997-08-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 90 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
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TYPE: PRT
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                                                                                                                                                                 TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-08-19
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/056,364
                        284 EMLFFTQLQVGLIQQWMVPTIQNSMK 309
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EMLFFTQLQVGLIQQWMVPTIQNSMK 26
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o. US20050244845A1
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                                                                                            Score 134; DB 9;
Pred. No. 1.3e-05
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Pred. No.
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FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SegWin99, version 1.04

SEQ ID NO 3820

LENGTH: 484

TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

US-10-467-657-3820
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PRIOR FILLING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR PPLICATION NUMBER: 60/056,366
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR PILING DATE: 1997-08-19
REMEDIATE: PSEQ ID NOS: 373
NUMBER OF SEQ ID NOS: 373
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 304
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US-10-467-657-3820
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-986-501-304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 4.5%; Score 118; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                        Matches
                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: FIEZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
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PRIOR APPLICATION NUMBER: US/10/621,363
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR APPLICATION NUMBER: 09/969,730
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                                                                                                                                                                   Local Similarity 19.2
nes 92; Conservative
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FILING DATE: 2000-10-06
APPLICATION NUMBER: 09/244,112
FILING DATE: 1999-02-04
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                                                                                                               131 WPAPCLVIAANVFAV------AAFQVEKRLAVGALTEQAGLLLHVANLATILCFPAA 181
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                                                                       WEMPLLSVEFALFFIVFLPIYWGFAKYPSVQNLLL--LAAGMGWLYHISPV----FAAI 57
                                                                                                                                                              4.4%; Score 114.5; DB 9; Length 484;
19.2%; Pred. No. 0.027;
Live 56; Mismatches 152; Indels 179; Gaps
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9 FVTEHEVCLSFVVENTANPDDAGAVESALFANAGGWNAPQRADMLLLASFASLMLLYPY 437	Db 379	п
13 FVGREFQGNYGNAAVWLSLIIGQPIAVLMYVHDY 476	Qy 443	0
319 RTQLNLMAAMVLSGIWHGYGWNFLIWGALHGTALALLNTGDRYFGRDALCRLKYLAPLSW 378	Db 3:	н
04 RTGVELASAFFHEYLVSVPLRMFRLWAFTGMMAQIPLAW 442	Qy 404	0
280 APLRAANIRAFWDKWHISLSTWIRDYIYIPLGGSKKGFL 318	Db 21	п
344 SCLNAVAELMQEGDREFYRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMA 403	Qy 3	_
230 FENPTQFDGWGVLAGVYGYTFQLFLDFSGYSDLVIGNAMLLGFRLPKNFS 279	Db 2:	н
304 IQNSMKPFKDMD-YSRIIERLLKLAVPNHLIWLIFFYWLFH 343	Ογ 3.	_
171 RAAAFKSTDGEQAGALAQIRTRRPRSP-VRPALAVSLILLGIAKKWWLAGILAENWVSPV 229	Db 1:	н
268	Qy 2	_
115 G-GAIDILMPLGLSYYTFQSVAYLVYCFRAPHAARFGWHELLLHLSFFPTVTSGPII 170	Db 1	н
229 GKKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNF 267	Оу 2:	^
58 IVLYSSCVYLLGELLRSDRESTRRFWLGCGIAASÍTVLGFFKYFDFFRPLIAQYAGK 114	В	-

Search completed: May 5, 2006, 12:46:20 Job time : 29 secs

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Result
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Perfect score:
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2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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Ygapop 10.0 , Ygapext
Egapop 6.0 , Egapext
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Sequence 5894, App
Sequence 314, App
Sequence 29256, A
Sequence 12886, A
Sequence 12898, A
Sequence 12899, Ap
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equence 46517,	Sequence 46504, A	equence 21, App	equence 7,	equence	e 350	equence 17,	equence 5, F	equence 3017	equence 1195	equence 33444,	equence 34424	equence 209, Ap	equence 33843,	equence 33355,	o.	equence :	Sequence 33281, A	e 3373	equence 12	e 20,	e 2571	nce 22,	1Ce 13,	e 12892,	ce 46522,	4649	290	1289	128	e 128	equence 1150	quence 12905,	quence 12900,	quence 12894,	equence 12888	92, Ap

ALIGNMENTS

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo
US-09-867-701-4664
US-10-659-800-6 (1-488) x US-09-867-701-4664 (1-452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-867-701-4664
                                                                                                                                                                                                                                        APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT APPLICATION NUMBER: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4664
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4664, Application US/09867701 Patent No. US20020132237A1 GENERAL INFORMATION:
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32.5%
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                               Gaps:
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Matches:
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239 285 299

359

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Sequence 5894, Application US/09867701

Patent No. US20020132237A1

GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Aglate, Paul A.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOUTWARE: FRSEUER for Windows Version 4.0

SEQ ID NO 5894

LENGTH: 371

TYPE: DNA
ORGANISM: Homo sapien
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Query Match:
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                                                                                                                  ValGluSerIleThrProValGlySerLeuLeuAlaLeuMetAlaHisThrIleLeuPhe
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AlaSerAlaGlyLysLysAlaSerSerAlaAlaAlaProHisThrValSerTyrProAsp
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 314
LENGTH: 433
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (428)
OTHER INFORMATION: n equals
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PUZO6
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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 pTrpTrp-AsnSerGluSerValThrTyrPhe---TrpGlnAsnTrp-AsnIleProVal
                                            SerCysLeuAsnAlaValAlaGluLeuMetGlnPhe-GlyAspArgGluPheTyrArgAs
                                                                                                                                                                              GluLeuAsnPheProArgSerProArgIl&ArgLysArgPheLeuLeuArgArgIleLeu
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                                                                                                                    LeuLysLeuAlaValProAsnHisLeuIl¢TrpLeuIlePhePheTyrTrpLeuPheHis
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APPLICANT: Hybeq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUE
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRA
FILE REFERENCE: 20411-756
CURRENT EDING DATE: 20410-07-30
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOPTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 29256
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(447)
OTHER INFORMATION: n = A
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                                                                                                                                 nAlaValAlaGluLeuMetGlnPheGlyAspArgGluPheTyrArgAspTrpTrpAsnSe
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                       gHisPheTyrLysProMetLeuArgArgGlySerSerLysTrpMetAlaArgThr 405
                                                                     rGluSerValThrTyrPheTrpGlnAsnTrpAsnIleProValHisLysTrpCysIleAr
                                                                                                                                                                         GGGCTTGTTTCTGCAGGACATGGACTACTCACGCATCATCAGCGCCCTCCTGAAGCTGGC
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Sequence 1286, Application US/10741600

| Publication No. US20050026169A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al.
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WIT TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF IFILE REFERENCE: CL001499
| CURRENT APPLICATION NUMBER: US/10/741,600
| CURRENT FILING DATE: 2003-12-22
| NUMBER OF SEG ID NOS: 73997
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEG ID NO 12886
| LENGTH: 201
| TYPE: DNA Homo sapiens
                                                                                                                                                                                                           Sequence 12898, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: MYCCARDIAL INFARCTION,
FILE REFERENCE: CLOO1499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT TILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12898
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Best Local Similarity:
Query Match:
                Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-741-600-12898
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                                                                                                                                                               ORGANISM: Homo
                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                 LENGTH: 201
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                                                                                                                                                            sapiens
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GENETIC POLYMORPHISMS ASSOCIATED WITH
MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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US-10-659-800-6 (1-488) x US-10-741-600-12898 (1-201)

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Sequence 1979, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

ITITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FASEUSEQ for Windows Version 3.0

SEQ ID NO 1979

LENGTH: 471
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Best Local Similarity:
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US-09-918-995-1979
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LOCATION: (1)...(471)
OTHER INFORMATION: n =
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ORGANISM: Homo sapiens
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                                                                                                                            PheHisSerCysLeuAsnAlaValAlaGluLeuMetGlnPheGlyAspArgGluPheTyr 361
                                                                                                                                                                                                                                                                                                                                          AspTyrSerArgIleIleGluArgLeuLeuLysLeuAla-----
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                                                                  ArgAspTrpTrpAsn---
                                                                                                    TTCCACTCCTGCCTGAATGCCGTGGCTGAGCTCATGCAGTTTGGAGACCGGGAGTTCTAC
                                                                                                                                                                              CCCCCACCTCCCTGCCAGGTCCCCAATCACCTCATCTGGCTCATCTTCTTCTACTGGCTC
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                                    CGGGACTGGTG-AGTGTCCCTGGGGTGTCCCTGGGGGCTGGGATGGGCCATGGTGTG
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CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 192
SEQ ID NO 192
LENGTH: 380
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1) ... (380)
OTHER INFORMATION: n = A,T,C or G
US-09-770-791-192
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Best Local Similarity:
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APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2029 (PARA-018PRV)
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APPLICANT: An, Yong
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                                                              ---AspMetAspTyrSerArgIleIleGluArgLeuLeuLysLeuAlaValProAsnHis
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LeuIleTrpLeuIlePhePheTyrTrpLeuPheHisSerCysLeuAsnAlaValAlaGlu
                                                                                                        GGATTTATAATAGAACAATATATAAATCCTATTGTCAGGAACTCCAAAGCATCCTTTGAAA 135
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Davis, Keith R.
Allen, Keith
                                    GGCGATCTTCTATATGCT-----ATTGAAAGAGTGTTGAAGCTTTCAGTTCCAAATTTA 189
                                                                                                                                                                                ATACGGAAGGGTTGGGTGGCTCGTCAATTTGCAAAACTGGTCATATTCACCGGATTCATG
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Kricker, Maja
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Haas, William David
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Hamilton, Carol M
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eaka, Joshua G.
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US-10-741-600-12894

; Sequence 12894; Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michale et al.

; TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WIT

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF D

; FILE REFERENCE: CL001499

; CURRENT APPLICATION UMBER: US/10/741,600

; CURRENT APPLICATION OF D

; CURRENT PAPELLONG DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FASTSEQ for Windows Version 4.0
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Publication No. US20050026169A1

GENERAL INFORMATION:
GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ.ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12888
US-10-741-600-12888
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US-10-741-600-12888
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                                                                              THEREOF
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Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECT
FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FASSISEQ for Windows Version 4.0

SEQ ID NO 12900

LENGTH: 201
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; TYPE: DNA
; ORGANISM: Homo s
US-10-741-600-12894
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Best Local Similarity:
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US-10-741-600-12900
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                         179
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                                         LeuThrGluGlnAlaGlyLeuLeuLeuHisValAlaAsnLeuAlaThrIleLeuCysPhe
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DETECTION AND USES

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RESULT 13
US-10-424-599-115051
Sequence 115051, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosea Thomas J
APPLICANT: Kovalic David K
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCB: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 115051
LENGTH: 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12905, Application US/10741600

Sequence 12905, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION: Michele et al.

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECT FILE REFERENCE: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF ESO ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12905

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens
Alignment Scores
                                    ; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone
US-10-424-599-115051
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Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS
TITLE OF INVENTION: MYCCARDIAL INFARCTION,
FILE REFERENCE: CL001499
CURRENT APPLICATION UNMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12887
LENGTH: 201
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US-10-741-600-12887
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US-10-659-800-6 (1-488) x US-10-741-600-12887 (1-201)
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AspTyrTyrValLeuAssTyrGluAlaProAlaAlaGluAla
                                                                              AlaAlaValTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTyrValHis
                                                                                                                                                               MetAlaGlnIleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsnTyrGlyAsn
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                                                       GCAGCTGTGTGGCTGTCGCTCATCATCGGACAGCCAATWGCCGTCCTCATGTACGTCCAC
                                                                                                                                        ATGGCTCAGATCCCACTGGCCTGGTTCGTGGGCCGCTTTTTCCAGGGCAACTATGGCAAC
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GENETIC POLYMORPHISMS ASSOCIATED WITH
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RESULT 15
US-10-741-600-12893
US-10-741-600-12893
Sequence 12893, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01499
CURRENT APPLICATION UNMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOUTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 12893
LENGTH: 201
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
US-10-741-600-12893
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Search completed: May Job time : 1157 Becs
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Pred. No.:
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                                                        GACTACTACGTGCTCAACTATGAGGCCCCAGCGGCAGAGGCC 164
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Post-processing: Minimum Match 0%
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -MODEL=frame+ p2h.model -DBv-xlp
-Q=/abss/ABSSWEB_spool/US10659800/runat_05052006_122310_17268/app_query.fasta_1
-DB=Issued_patents_NA -OPMT=fastap_-SUFFIX=p2n.szln500.rni -MINMATCH=0.1
-DB=Issued_patents_NA -OPMT=fastap_-SUFFIX=D-2n.szln500.rni -MINMATCH=0.1
-LOOPCL=0 -LOOPCXT=0 -UNITS=bbts_-START=1 -END=-1 -MATRIX=bbosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=500 -HOST=bbs02p
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1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*

9: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
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**Ygapop 10.0 , Ygapext
**Ygapop 6.0 , Fgapext
**Pgapop 6.0 , Delext
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Sequence 13, Appl
Sequence 20, Appl
Sequence 14231, A
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Sequence 4, Appli
Sequence 3, Appli
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ALIGNMENTS

RESULT 1 US-09-326-203A-13

Sequence 13, Application US/09326203A Patent No. 6444876

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Query Match:
DB:
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Best Local Similarity:
                                                                          Score:
                                                                                            Pred. No.:
                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                                            TITLE OF INVENTION: Acyl-CoA:Cholesterol Acy
TITLE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1998-11-12
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                       ; SOFTWARE: Pat
; SEQ ID NO 13
; LENGTH: 299
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 1977...
GENERAL INFORMATION:
APPLICANT: Lasener, Mike
APPLICANT: Ruezinsky, Diane
APPLICANT: Nezinsky, Diane
                                                                                                                                                                   TYPE: DNA
ORGANISM: murine
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SEQ ID NO 20
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LOCATION: (46) TOTHER INFORMATION: n at
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ORGANISM: Caenorhabditis
FEATURE:
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                                                                                                                                                          101 AlaArgLeuPheLeuGluAsnLeuIleLysTyrGlyIleLeuValAspProIleGlnVal 120
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138 IleAlaAla 140
                                                                          121 ValSerLeuPheLeuLysAspProHis-----SerTrpProAlaProCysLeuVal 137
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                                       ATCTCAACGTTTGTTGAGCATCACTACTCAATTTGGAGCTGGCCAAATCTTGCTCTCATC
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                  Alignment Scores: Pred. No.:
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SEQ ID NO: 5
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Glycine max
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; ORGANISM: Homo
US-09-621-976-14231
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                                                                                                                                                                                                                                                                                    APPLICANT: Lassner, Mike
APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-11-12
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SOFTWARE: Patent.pm
SEQ ID NO 14231
LENGTH: 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
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CURRENT FILING DATE: 2000-07-21
                                                                                                 NAME/KEY: misc feature
LOCATION: (192]..(263)
OTHER INFORMATION: n at
OTHER INFORMATION: 239,
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RESULT 6
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/172,711
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PERL Program
SEQ ID NO 58
LENGTH: 225
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APPLICANT: Zweiger, Gary B.
APPLICANT: Panzer, Scott R.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: MONITORING TOXICOLOGICAL RESPONSES
FILE REFERENCE: PA-0011 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 225
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: 28, 59, 65, 73, 79, 84, 88
OTHER INFORMATION: a or g or c or t, unknown, or other
FEATURE: -
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                                                                                                145
                               205
                                                    222 ArgAlaLysAlaAlaSerAla 228
                                                                                                                      204 LeuPheLeuLysLeuPheSerTyrArgAspValAsnSerTrpCys-----ArgArgAla 221
                                                                                                                                                                                     184 LeùLeuValGluSerIleThrProValGlySerLeuLeuAlaLeuMetAlaHisThrIle
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                               AAGGCCAAAGCTGTGTCTGCA 225
                                                                                                ATETTCCTCAAGCTTTTCTCCTACCGGGATGTCAATCTGTGGTGCCGCCAGCGAAGGGTC
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Matches:
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GENERAL INFORMATION:
APPLICANT: Lassner, Mike
APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acy
TITLE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-01-05
PRIOR FILING DATE: 1998-11-12
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SEQ ID NO 7
LENGTH: 253
TYPE: DNA
ORGANISM: Zea 1
                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09326203A Patent No. 6444876 GENERAL INFORMATION:
              SOFTWARE:
SEQ ID NO 4
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                                                APPLICANT: Lassner, Mike
APPLICANT: Ruezinsky, Diane
APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Acid Sequences
TITLE OF INVENTION: Acid Sequences
TITLE REFERENCE: 17045/00/WO
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR PILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-01-12
NUMBER OF SEQ ID NOS: 46
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LENGTH: 267
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                                 PatentIn Ver. 2.1
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SOFTWARE: Patentin ver. 2.1

SEQ ID NO 3

LENGTH: 234

TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc_feature
LOCATION: (24)...(60)
OTHER INFORMATION: n at positions 24
US-09-326-203A-3
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                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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                               US-10-659-800-6 (1-488) x US-09-326-203A-3 (1-234)
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Pred. No.:
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US-09-326-203A-3
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Best Local Similarity:
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; ORGANISM: G1
US-09-326-203A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related
TITLE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
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                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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LeuThrTyrArgAspLeuTyrTyrPheLeuPheAlaPro-ThrLeuCysTyrGluLeuAs
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APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Jeffrey R.Shuster
APPLICANT: Ib Groth Clausen
APPLICANT: Ib Groth Clausen
APPLICANT: Ib Groth Clausen
TITLE OF INVENTION: Expression
FILE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT APPLICATION NUMBER: 09/273,623
EARLIER APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF 580 ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1684
LENGTH: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Fusarium FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(200)
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                                                                                                                                                                                                         ArgArgAlaArgAlaLysAlaAlaSerAlaGlyLysLysAlaSerSerAlaAlaAlaPro 238
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APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Rel
TITLE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
CURRENT FILING DATE: 19045/00/WO
CURRENT FILING DATE: 1909-06-04
PRIOR APPLICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1908-06-05
PRIOR APPLICATION NUMBER: 60/08,389
PRIOR APPLICATION NUMBER: 60/08,389
PRIOR FILING DATE: 1908-11-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.1
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US-09-326-203A-16
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Best Local Similarity:
Query Match:
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                                               SEQ ID NO 10
LENGTH: 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 447
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                               TYPE: DNA
 FEATURE:
                 ORGANISM: Zea mays
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                               US-10-659-800-6 (1-488)
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US-09-252-991A-11268
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Best Local Similarity:
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APPLICANT: MAXC J. RUBENFIELD et al.
APPLICANT: MAXC J. RUBENFIELD et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 11268
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Pseudomonas
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LOCATION: (6)..(321)
OTHER INFORMATION: n at positions 6, 14, 16, 18, 32, 67, 71,
OTHER INFORMATION: 83, 85, 94, 107, 111, 170, 176, 180, 204,
OTHER INFORMATION: 206, 207, 208, 209, 261, 289, 296, 301, 30
OTHER INFORMATION: and 321 is unknown
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILLE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Best Local Similarity:
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Sequence 10793, Application US/05
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acid
FILE REFERENCE: File Reference:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 465
TYPE: DNA
ORGANISM: Pseudomonas
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                                                                                                                                                               GlyAspAlaGlyValGlySerGly 62
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   acids and proteins
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Matches:
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                 Drosophila melanogaster
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; ORGANISM: Drosophila
US-09-270-767-10793
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10793
LENGTH: 485
                                                                                                                         GENERAL INFORMATION:
                                                                                                                                    Sequence 6, Application Patent No. 6444876
    PRIOR APPLICATION NUMBER:
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Matches:
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US-10-659-800-6 (1-488) x US-09-270-767-10793 (1-485)
APPLICANT: Lassner, Mike
APPLICANT: Lassner, Mike
APPLICANT: Ruezinsky, Diane
APPLICANT: Ruezinsky, Diane
APPLICANT: Ruezinsky, Diane
TITLE OF INVENTION: Acyl-COA:Cholesterol Acyltransferase Related
TITLE OF INVENTION: Acid Sequences
FILE REFERENCE: 17045/00/WO
CURRENT APPLICATION NUMBER: US/09/326,203A
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 CysArgArgAlaArgAlaLysAlaAlaSerAla 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 ValPheAlaValAlaAlaPheGlnValGluLysArgLeuAlaValGlyAlaLeuThr---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATGGACATGCTGTAATAAAACAATTGAAGACCATAAACCTAATTGGTCAAGTGCTCAAG
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; PRIOR FILING DATE: 1998-06-05; PRIOR APPLICATION NUMBER: 60/108,389; PRIOR FILING DATE: 1998-11-12; NUMBER OF SEQ ID NOS: 46; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 6; LENGTH: 257; TYPE: DNA; ORGANISM: Glycine max US-09-326-203A-6
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Best Local Similarity:
Query Match:
DB:
Search completed; May 6, 2006, 13:07:20 Job time : 381 secs
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238 TTCATCCCT 246
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                                                                                                            418 ---LeuValSerValProLeuArgMetPheArgLeuTrpAlaPheThrGlyMetMetAla 436
                                                                                                 202 AAGCTTCTTCA----
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Matches:
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Result
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=Abse/ABSSWEB spool/US10659800/runat 05052006 122308 17225/app_query.fasta_1
-Q=Abse/ABSSWEB spool/US10659800/runat 05052006 122308 17225/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.szlm500.rst -MINMATCH=0.1 -LOOPCI=0.
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bitosum62 -TRANS=human#0.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-LOOPEXT=0 DOCALIGN=200 -THR SCORE=0t -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=500
-MOST=abse02h -USER-US10659800 @CGN 1 1 5315 @runat 05052006 122308 17225
-NCPU=6 -ICPU=3 -NO MARP -NEG SCORES=0 -WAITT-DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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BM743182 K-EST0016
AA430536 Zw21a05.r
BG078967 H3034B09-
AW446985 B8026 MAR-
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REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM ACCESSION VERSION FEATURES COMMENT DEFINITION CZ559383 HMA103 Ba Email: info@baygenomics.ucsf.edu Sequence tag generated by 5' RACE of total RNA from gene trap Ex Sequence ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. mRNA sequence. CZ559383 CZ559383.1 GI:66858688 http://baygenomics.ucsf.edu/cgi,bin/BaySearch.py?OPTION=EXACT&TYPE= CELL_LINE&KEY=HMA103 Contact: BayGenomics Bay Area Functional Genomics Cohsortium (BayGenomics) http://baygenomics.ucsf.edu/ Unpublished (2001) BayGenomics. Mus musculus (house mouse) (bases 1 to 487) 83 487 bp mRNA linear GSS 01-JUN-BayGenomics Gene Trap Library pGTILxf Mus musculus cDNA, Gene Trap. /organism="Mus musculus" /mol_type="mRNA" ocation/Qualifiers GSS 01-JUN-2005 Euteleostomi;

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Kim, Y.S.
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Kim, N.S., Hahn, Y.,
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Oh,K.J., Cheong,J.E., Sohn,F
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Kim, Y.S.
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Tel: +82-42-860-4470
Fax: +82-42-860-4409
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                                                                                                                                                                      /note=forgan: Stemach; Vector: pTZ18RP1; Site 1: EcoRI;
/note=forgan: Stemach; Vector: BAR) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector: The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheong, J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SNU-1"
/lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S4SNU1-6-D08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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100.0%
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BM743182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.

1 (bases 1 to 452)

1 (lbases 1 to 452)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jos:
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,T., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA430536
452 bp mRNA linear EST 09-NOV zw21a05.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:769904 5' similar to TR:Gl066810 Gl066810 ACYL-COENZYME
                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further Insert Length: 1033 Std Error: 0.00 Seg primer: -28m13 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHOLESTEROL ACYLTRANSFERASE. ;,
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/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5979779"
/db_xref="taxon:9606"
                                                       sex="Female"
                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                clone="IMAGE: 769904"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 467)
Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray
                                                                                                                                                                     H3034B09-5 NIA Mouse 15K cDNA
H3034B09 5', mRNA sequence
BG078967
BG078967.2 GI:40011342
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                                                                                                                                         Mus musculus
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This clone set has been freely distributed to the community. visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.plate: H3034 row: B column: 09
Seg primer: -21M13 Reverse
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AspArgGluPheTyrArgAspTrpTrpAsnSerGluSerValThrTyrPheTrpGlnAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone ib="WIA Mouse 15K cDNA Clone Set"
/clone ib="WIA Mouse 15K cDNA Clone Set"
/note="Vector: psport1; Site_1: Sall, Site_2: Not1; This
clone is among a rearrayed set of 15,447 clones from 11
embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5
embryos, and E12.5 femále mesonephros/gonad) and one
newborn ovary cDNA library. Average insert size 1.5 kb.
All source libraries are cloned unidirectionally with
Oligo(dT)-Not primers. References include: (1)
Genome-wide expression profiling of mid-gestation
placenta and embryo using a 15,000 mouse developmental
cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97:
9127-9132; (2) Large-sdale cDNA analysis reveals phased
gene expression patterns during preimplantation mouse
develolpment, 2000, Development, 127: 1737-1749; (3)
Genome-wide mapping of unselected transcripts from
extraembryonic tissue of 7.5-day mouse embryos reveals
enrichment in the t-complex and under-representation on
the X chromosome, 1998, Hum Mol Genet 7: 1987-1978."
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'dev_stage="Clones arrayed from a variety of cDNA
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/db_xref="niaEST:H3034B09-5"
/db_xref="taxon:10090"
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PO Box 166, Clay Ce
Tel: 402 762 4366
Fax: 402 762 4390
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Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR PRIMETS
FORWARD: AGGAAACAGCTATGACCAT
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Smith, T.P.L., Gross
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Box 166, Clay Center, NE 68933-0166, US
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le pass sequencing. Bases called and trimmed with phred
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Mus musculus
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata; Clires; Glires; Rodentia;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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uq98dil.x1 NCI CGAP Mam10 Mus
similar to TR:Q9Z2A7 Q9Z2A7 DI
sequence.
                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D.,
Gilbort Smith, Ph.D., William Muller, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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     Possible reversed clone:
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:947054
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National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
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 GlnProIleAlaValLeuMetTyrValHisAspTyrTyrValLeuAsnTyrGluAlaPro
                                 GGCCGATTCTTCCAAGGGAACTATGGCAATGCAGCTGTGTGGGTGACACTCATCATTGGG
                                                   GlyArgPhePheGlnGlyAsnTyrGlyAsnAlaAlaValTrpLeuSerLeuIleIleGly
                                                                                                                 ACAGGAGTATTTTTGACCTCAGCCTTCTTCCATGAGTACCTAGTGAGCGTTCCCCCTGCGG
                                                                                                                                                                                                                     CysIleArgHisPheTyrLysProMetLeuArgArgGlySerSerLysTrpMetAlaArg
                                                                                                                                                                                                                                                                                                                                               TGTCTCAATGCTGTGGCAGAGCTTCTGCAGTTTGGAGACCGCGAGTTCTACAGAGATTGG
                                                                                              ATGTTCCGCCTCTGGGCATTCACAGCCATGATGGCTCAGGTCCCACTGGCCTGGATTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="Soares mammary gland NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="female (lactating)"
tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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744.00
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Matches:
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DB:
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Best Local Similarity:
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          srpb2-00118-d4
CB801052
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AMGNNUC:SRPB2-00118-D4-A srpb2
srpb2-00118-d4 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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                                                                                                                                                                                                    HisSerCysLeuAsnAlaValAlaGluLeuMetGlnPheGlyAspArgGluPheTyrArg
                                                                                                                                                                                                                                                          LeuLeuLysLeuAlaValProAsnHisLeuIleTrpLeuIlePhePheTyrTrpLeuPhe
                                                                                                                                                                                                                                                                                                           ThtIleGlnAsnSerMetLysProPheLysAspMetAspTyrSerArgIleIleGluArg
 LeuArgMetPheArgLeuTrpAlaPheThrGlyMetMetAlaGlnIlePro 439
                                         AlaArgThrGlyValPheLeuAlaSerAlaPhePheHisGluTyrLeuValSerValPro 422
                                                                                               Ly&TrpCysIleArgHisPheTyrLysProMetLeuArgArgGlySerSerLysTrpMet
                                                                                                                                 GACTGGTGGAATGCTGAGTCTGTCACCTACTTTTGGCAGAACTGGAATATCCCCCGTGCAC
                                                                                                                                                                                      CACTCATGTCTCAATGCTGTGGCAGAGCTCCTGCAGTTTGGAGACCGCGAGTTCTACAGG
                                                                                                                                                                                                                                         CTCTTAAAGCTGGCGGTCCCCAACCATCTGATATGGCTCATCTTCTATTGGCTTTTC
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pen EST Program
pen Rat EST Program
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e: 00118 row: d column:
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                                                                                rgcatcagacacttctacaagcctatgctcagactgggcagcaacaaatggatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="prostate tissue"
/clone_Tib="sarpb2 (10220)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; rat
prostate normalized double selected poly(A+) mRNA size
fraction > 1 kb"
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/db_xref="taxon:10116"
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|mol_type="mRNA"
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AUTHORS
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VERSION
KEYWORDS
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CO260334
                                                                                                                                            Query Match:
                                                                                                                                                                                      score:
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 62
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US-10-659-800-6 (1-488) x CO260334 (1-407)
                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                       Similarity:
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4132042 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim_alt ', -trim_fasta. Vector identified by cross match using options -minmatch 12 -minscore 18 plate: 57 row: F column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2004)
Contact: Richard G. Baumann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 407)
Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van
Matukumalli, L.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLDG 162: BARC-EAST, Beltsville, Tel: 3015048604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine Functional Genomics Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: CCTATTTAGGTGACACTATAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rbaumann@anri.barc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 3015048744
                      ProAsnHisLeuIleTrpLeuIlePhePheTyrTrpLeuPheHisSerCysLeuAsnAla
                                                                                                    LysProPheLysAspMetAspTyrSerArgIleIleGluArgLeuLeuLysLeuAlaVa1
AAGCCCTTCAAGGACATGGACTATTCCCGCATCGTGGAGCGCCTCCTGAAGCTGGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 407.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Intestine; Vector: pCMVSport6.1; Site_1: Not1; Site_2: EcoRI; Normalized cow cDNA intestinal library in pCMVSport6.1, constructed from equimolar mRNA pools derived from 5 sburces, 4 lactating intestinal, 1 neconatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TONA"'
/clone_lib="BARC 8BOV"
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/clone="8BOV_57F07"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="Holstein"
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738.00
97.8%
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8BOV_57F07
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REFERENCE
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BF733499/c
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1 (bases 1 to 459)

1 (bases 1, Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Dias Neto,E., Garcia Correa,R., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-AN0063-
081000-011-B03&t3=2000-10-08&t4=1)
Seq.primer: puc 18 forward
Seq.primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
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BF733499
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Tel: +55-11-2704922
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               /note=Torgan: amnion_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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AMGNNUUC:TRXP1-00014-D10-A TXXP1
clone trxp1-00014-d10 5', mRNA 8
CB771505
                                                                                                                          Amgen, Inc
one Amgen Center Drive, Thousand Oaks,
Tel: 805_447-4881
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Amgen EST Program
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Unpublished (2003)
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murodea; Muridae; Murinae; Rattus.
                                                                                                                                                                                        Contact: Dan Fitzpatrick
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00014 row: d
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Location/Qualifiers
                                                                      organism="Rattus norvegicus"
                        clone="trxp1-00014-d10"
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                                                                                                        Amgen, Inc
One Amgen Center Drive, Thousand
Tel: 805 447-4881
Plate: 00005 row: c column: 5.
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Mammalia; Eutheria; Euarchontglires; Glires; Rodentia;
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AMGNNUC:TRXP1-00005-C5-A trxp1 (1
trxp1-00005-C5 5', mRNA sequence
CB775155
CB775155.1 GI:29863546
                                                                                                                                                           Contact: Dan Fitzpatrick
                                                                                                                                                                       Unpublished (2003)
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/organism="Rattus norvegicus"
/mol type="mRNA"
/db_xref="taxon:10116"
/clone="trxp1-00005-c5"
/tissue_type="prostate"
/clone_lib="trxp1 (10556)"
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/note="Vector: pYYA-41L; Site_1: HindIII; Site_2: NotI;
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US-10-659-800-6 (1-488) x CB775155 (1-391)
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                 Tel: +55-11-2707001

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-ST0233-251199-041-g07&t3=1999-11-25&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 494.
                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 494)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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QV4-ST0033-251199-041-g07
AW391923
AW391923.1 GI:6896582
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                              Homo sapiens
                                          Homo sapiens (human)
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/clone lib="ST0233"
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
/note="Organ: stomach; Vector: puc18; Site 1: SmaI;
/note="Organ: stomach; Vector: puc18; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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Contact: Kim YS
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   ValGlyAlaLeuThrGluGlnAlaGlyLeuLeuLeuHisValAlaAsnLeuAlaThrIle 175
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US-10-659-800-6 (1-488) x BM857224 (1-430)
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
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Plate: 78 row: D column: 11
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                                       LeuValIleAlaAlaAsnValPheAlaValAlaAlaPheGlnValGluLysArgLeuAla 155
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNU520-78-D11"
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/cell_line="SNU-520"
/lab_host="Top10F'"
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196 LeuAlaLeuMetAlaHisThrIleLeuPheLeuLysLeuPheSerTyrArgAspValAsn 215	LeuAlaLeuMetAlaHisTh	196	Ş
303 CTGTGTTTCCCAGCGGCTGTGGTCTTACTGGTTGAGTCTATCACTCCAGTGGGCTCCCTG 362	CTGTGTTTCCCAGCGGCTGT	303	D
176 LeuCysPheProAlaAlaValValLeuLeuValGluSerIleThrProValGlySerLeu 195	LeuCysPheProAlaAlaVa.	176	Ş
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-Q=/abss/ABSSWEB spool/US10659800/runat_05052006_122305_17180/app_query.fasta_1
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.szlm500.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=500
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=500
-HOST=abss02p -USER=US10659800 @CGN 1 1 1929 @runat 05052006 122305 17180
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WĀRN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Aad40443 Bovine di
Abl82916 Human ova
Aas41185 cDNA enco
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ALIGNMENTS

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RESULT 1
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ID ABL8
Algate PA, Harlocker SL,
                                                                                          06-DEC-2001.
                                                                                                                                            Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss
                                                                                                                                                            Human ovarian cancer related cDNA clone SEQ ID NO:4664.
       WPI; 2002-122075/16
                                                         26-MAY-2000; 2000US-0207484P
                                                                          29-MAY-2001; 2001WO-US017756.
                                                                                                           WO200192581-A2
                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-659-800-6 (1-488)
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                    MetLeuArgArgGlySerSerLysTrpMet
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RESULT

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production traits which comprises determining the diacylglycerol acyltransferase (DGAT1) genotypic state of the bovine, wherein the DGAT1 gene and polymorphisms have been found to be associated with such improved milk production traits. The method is useful for selecting a bovine having a desired DGAT1 genotypic state. It is also useful for the identification and selection of a bovine having one of the polymorphisms in its DGAT1 gene. Milk produced from selected bovine which is useful for making a dairy product provides a beneficial health effect. An antibody to the protein having DGAT1 activity is useful for inhibiting the activity of bovine DGAT1 in a lactating bovine so as to modulate milk production and/or milk solids content. DGAT1 nucleic acid and its fragments are useful in the farming industry. They are also useful to generate transgenic animals which are useful to investigate the molecular
                                                                                                                                                                                                                                                                                                       Georges
Ford CA,
                                                                                                                                                                                                                        Determining genetic merit of a bovine with respect to milk composition and volume for improved milk production, comprises determining the diacylglycerol acyltransferase gene genotypic state of the bovine.
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06-DEC-2000;
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DGAT1; polymorphism;
                                                                                                                                                                         The invention relates to a method of genotyping
                                                                                                                                                                                                 Disclosure; Page 41-42; 128pp; English,
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(COPP/)
(GRIS/)
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(FORD/)
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\, Spelman
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FORD C A.
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SNELL R G.
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polymorphism; farming industry; transgenic; enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                SPELMAN R J.
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2000NZ-00508662.
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  Algate PA,
                                                                                              26-MAY-2000; 2000US-0207484P
                                                                                                                                             29-MAY-2001; 2001WO-US017756.
                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian cancer related cDNA clone SEQ ID NO:5894.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a composition (I) comprising: carriers CC and immunostimulants; and a polypeptide (II) of a ovarian tumour CC polypeptide encoded by a polynuclectide (III) having a cDNA sequence (S1) CC from the 10912 nuclectide sequences as given in ABL77023 to ABL87934, CC (III) encoding (II) having a sequence (S2), a T cell population of (II), CC or antigen presenting cells that express (II). (I) has cytostatic CC activity. An oligonuclectide (IV) that hybridises to (S1) can be used for CC detecting ovarian cancer in a patient s biological sample preferably CC serum or ovarian tissue. The method comprises contacting a biological CC sample from a patient with (IV), detecting the amount of polynuclectide hybridising to (IV) and comparing the amount to a predetermined cutoff CC value and thereby detecting ovarian cahcer in the patient, where the CC amount of polynuclectide hybridising the IV) is detected preferably by CC polymerase chain reaction (PCR). (I) comprising (II) and/or (II) is CC useful for stimulating and/or expanding T cells specific for an ovarian CC tumour protein comprising contacting T cells specific for an ovarian CC useful in design and preparation of ribozyme molecules for inhibiting CC expression of the tumour polypeptides and proteins in tumour cells; and CC to isolate a full length gene from a stitable library e.g., a tumour cDNA CC library using well known techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 371
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                                                                                                                                                                                AsnPheProArgSerProArgIleArgLyBArgPheLeuLeuArgArgIleLeuGluMet
                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLysLeuPheSerTyrArgAspValAsnSerTrpCysArgArgAlaArgAlaLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGluSerIleThrProValGlySerLeuLeuAlaLeuMetAlaHisThrIleLeuPhe
                                                                    AsnSerMetLys
                                                                                                                                                                                                                                                         AATCTGACCTACCGCGATCTCTACTACTTCCTCTTCGCCCCCACCTTGTGCTACGAGCTC
                                                                                                                                                                                                                                                                            AsnLeuThrTyrArgAspLeuTyrTyrPhéLeuPheAlaProThrLeuCysTyrGluLeu
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                                    AACTCCATGAAG
                                                                                                          CTGTTCTTCACCCAGCTCCAGGTGGGGCTGATCCAGCAGTGGATGGTCCCCACCATCCAG
                                                                                                                                 LeuPhePheThrGlnLeuGlnValGlyLeuIleGlnGlnTrpMetValProThrIleGln
                                                                                                                                                                                                                                                                                                                               GCCTCTGCAGGGAAGAAGGCCAGCAGTGCTGCTGCCCCGCACACCGTGAGCTACCCGGAC
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17-DEC-2001 (fire CDNA encoding nove Human; oxidoreduct ligase; hyperprolidated diserved inflammatory discolar encoding nove Human; oxidoreduct ligase; hyperprolidated diserved inflammatory discolar encoding nove Homo sepiens. W0200155301-A2. 02-AUG-2001; 20001 31-JAN-2000; 20001 24-FEB-2000; 20001 24-FEB-2000; 20001 25-MAR-2000; 20001 17-MAR-2000; 20001 17-MAR-2000; 20001 17-MAR-2000; 20001 17-MAR-2000; 20001 17-MAR-2000; 20001 17-MAR-2000; 20001 11-JUL-2000; 20001 11-JUL-2000; 20001 11-JUL-2000; 20001 11-JUL-2000; 20001 11-JUL-2000; 20001 11-JUL-2000; 20001 11-AUG-2000; 20	AAS41185 sta AAS41185;
codding novel human enzyme polypeptide #401. oxidoreductase nnzyme; transferses; hydrolase; lyase; isomerase; hyperproliferative disorder; memondeficiency disorder; elated disorder; neurological disorder; neurological disorder; disorder; retabolic disorder; petrological dis	standard; cDNA; 433 BP.
	
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14-SEP-2000 14-SEP-2000 14-SEP-2000 14-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 20-OCT-2000 21-NOV-2000 20-OCT-2000 21-NOV-2000 21-NOV-2000 08-NOV-2000 08-NOV-2000 01-NOV-2000	0000
2000US-023399P. 2000US-0232401P. 2000US-0233063P. 2000US-0233063P. 2000US-0233063P. 2000US-023363P. 2000US-0234274P. 2000US-0234274P. 2000US-0234299P. 2000US-0234299P. 2000US-0234293P. 2000US-023536P. 2000US-023536P. 2000US-02353703P. 2000US-02353703P. 2000US-02353703P. 2000US-02353703P. 2000US-02353703P. 2000US-0237703P. 2000US-0237703P. 2000US-0237703P. 2000US-0237703P. 2000US-0237703P. 2000US-0237703P. 2000US-0237703P. 2000US-023478P. 2000US-023478P. 2000US-024677P. 2000US-024921P. 2000US-02492P. 2000US-02492P. 2000US-02492P. 2000US-02492P.	000US-0232081 000US-0231968 000US-0232397 000US-0232398

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                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to the isolation of novel human enzyme CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences CC encoding them. The enzyme polypeptides of the invention may comprise the CC functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the CC disorders including hyperproliferative disorders (e.g. cancer), CC disorders including hyperproliferative disorders (e.g. cancer), CC arthritis), neurological disorders (e.g. AlDS) autoimmune disorders (e.g. atthritis), neurological disorders (e.g. AlDS) autoimmune disorders (e.g. atthritis), neurological disorders (e.g. AlDS) autoimmune disorders (e.g. atthritis), neurological disorders (e.g. Alzheimer's disease), metabolic CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. atthra), CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. hasmatory disorders (e.g. infertility) and CC invention can also be used in gene therapy. AAS40785-AAS41684 represent CC convention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly continued at the polynopublished pot_sequences.
                                                                                                                                                                                                                                                                                                                                        Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                Sequence
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 CTGAAGCTGGCGGTCCCCAATCACCTCATCTGGCTCATCTTCTTCTACTGGCTCTTCCAC
               LeuLysLeuAlaValProAsnHisLeuIleTrpLeuIlePhePheTyrTrpLeuPheHis
                                                       ATCCAGAACTCCATGAAGCCCTTCAAGGACATGGACTACTCACGCATCATCGAGCGCCTC
                                                                        IleGlnAsnSerMetLysProPheLysAspMetAspTyrSerArgIleIleGluArgLeu
                                                                                                                GAGATGCTGTTCTTCACCCAGCTCCAGGTGGGGCTGATCCAGCAGTGGATGGTCCCCACC
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2000US-0256719P.

2000US-0251479P.

2000US-0251866P.

2000US-0251868P.

2000US-0251869P.

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2000US-0180628P
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2000US-0186350P
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2000US-02148867P
2000US-0214886P
2000US-0216847P
2000US-0217487P
2000US-0218290P
2000US-0218290P
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P-PSDB; ABB10426.
                                                                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention provides human cDNAs, proteins and related s. These can be used in the treatment of neural, immune system cular, reproductive, gastrointestinal, pulmonary, cardiovasculal and proliferative disorders and inflammation. The present s cDNA of the invention
                                                                                                                                                                                                                                                                                                                                                                                                          Scores:
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GluLeuAsnPheProArgSerProArgIl&ArgLysArgPheLeuLeuArgArgIleLeu
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04-FEB-2000;
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2000US-0216647P.
2000US-021748PP.
2000US-021749FP.
2000US-021749FP.
2000US-0220964P.
2000US-0224519P.
2000US-022526FP.
2000US-0225275P.
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US-10-659-800-6 (1-488) x ABV83985 (1-433)

264 GluLeuAsnPheProArgSerProArgIleArgLysArgPheLeuLeuArgArgIleLeu 283

Percent Similarity: Best Local Similarity: Query Match:

6.04e-48 603.50 87.2% 85.1% 23.3%

Mismatches: Indels: Gaps:

Length: Matches: Conservative:

433 126 3 12 12

Alignment

Scores:

No . :

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The invention relates to novel genes (ABV83682-ABV84101) and proteins CC (ABP66710-ABP67129) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are CC isolated from a range of human tissues disclosed in the specification. CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing CC infectious diseases such as myocardial ischaemias; (d) wound healing CC infectious diseases such as viral, bacterial, fungal and parasitic CC infectious diseases such as viral, bacterial, fungal and parasitic CC infections. Note: The sequence data for this patent did not form part of CC the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptide useful for diagnosis, prognosis, prevention, treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.
Sequence
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
                                  Claim 1; SEQ ID NO 29256; 44pp; English
                                                        New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
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(STAC/)
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Best Local Similarity:
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The invention relates to a novel nucleic acid of Arabidopsis thaliana comprising a sequence capable of hybridising under stringency to one capable of hybridising under stringency to one capable of produce in the specification (ABQ85131-ABQ86129). The nucleic acid sequences are useful to identify homologous or related genes, to produce compositions that modulate expression or function of the encoded protein, to map functional region of the protein, to study associated physiological pathways, to genetically manipulate cells and plants. The encoded products are useful oscreen for biologically active agents such as fungicides or
                                                                                                                                                                                                                                                                                                                  New nucleic acid sequences of Arabidopsis thaliana products are useful to produce transgehic plants, t biologically active agents such as fungicides and i
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, Page A, M
Kricker M,
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Ledford BL,
[, Davis KR,
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to identify

regions

insecticides and to elucidate biochemical pathways

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RESULT 10
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y Match:
                                                                                                                                                                                                         Acyl-CoA:cholesterol acyltransferase; ACAT; ACAT-like protein; sterol; ester; triacylglycerol; fatty acyl-CoA; lipid composition; plant cell; diacylglycerol acyltransferase; DAGAT; triglyceroide; cancer; diabetes; cardiopulmonary disease; heart failure; atherosclerosis; adipocytosis; leukaemia; skin carcinoma; fibroblastoma; metabolic disorder; obesity; abnormal lipid metabolism; abnormal fat absorption;
                                         05-JUN-1998;
12-NOV-1998;
                                                                                 04-JUN-1999;
                                                                                                             09-DEC-1999.
                                                                                                                                       W09963096-A2
                                                                                                                                                                                                                                                                                                      DNA encoding a protein related to ACAT-like proteins.
                                                                                                                                                                                                                                                                                                                                   27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                              AAZ45382
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               (CALJ ) CALGENE LLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATGTGTGGCTCTGCATGTTCTACTGCTTCTTCCACCTTTGGTTAAACATATTGGCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGATCTTCTATATGCT-----ATTGAAAGAGTGTTGAAGCTTTCAGTTCCAAATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AspMetAspTyrSerArgIleIleGluArgLeuLeuLysLeuAlaValProAsnHis
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                                                                                                                                                                                             secretion; adipogenesis; ss.
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98US-0108389P.
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a protein related to acyl-CoA:cholesterol cc acyltransferase (ACAT) related proteins. ACAT-like proteins are active in ct the formation of a sterol, ester and/or triacylglycerol from a fatty acyl cook and sterol and/or diacylglycerol substrate. DNA encoding an ACAT-C like protein can be used for modifying the lipid composition of plant cells. The ACAT-like protein has diacylglycerol acyltransferase (DAGAT) activity, and so the synthesis of triglycerides can be suppressed or corrected using the DNA. The protein can be used to produce plant oils contentify antagonists and agonists of DAGAT activity. Such agonists and content associated with DAGAT activity, including diseases associated with Cancer, diabetes, cardiopulmonary diseases associated with Cancer, cardiopulmonary diseases e.g. heart failure, including cancer, diabetes, cardiopulmonary diseases associated with abnormal lipid metabolism, and diseases associated with abnormal lipid metabolism, and diseases associated with abnormal lipid metabolism, and diseases associated with abnormal lipid
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                                                                                        WO200061771-A2
                                                                                                                                                                                                                                                                  Acyl CoA:cholesterol acyltransferase;
                                                                                                                                                                                                                                                                                                                           Mouse acyl CoA:cholesterol acyltransferase EST DNA sequence
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                                                                                                                                                                                                                                   tocopherol; phytosterol; phytostanol;
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                                                                                                                                                                                                                                                                  ACAT; transgenic plant; sterol;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of mouse acyl CoA:cholesterol acyltransferase (ACAT) expressed sequence tag (RST) DNA sequence II.

Comouse ACAT EST DNA sequence I is given in AAA88844. Sterol October ACAT EST DNA sequence I is given in AAA88844. Sterol October Strom cholesterol and long chain fatty acids. Recombinant constructs of the invention are used to alter the biosynthesis and accumulation of sterols and tocopherols in transgenic plants. Seeds of such plants may contain elevated levels of stoostanol and/or its esters, and their esters. The seeds may also contain the novel sterol and their esters. The seeds may also contain the novel sterol brassicastanol. Oil obtained from the seeds can be used in food and pharmaceutical compositions to lower levels of low density lipoprotein cholesterol in blood serum. ACAT enzymes can be used in the present invention to produce elevated levels of phytosterol and/or phytostanol
               Lolium perenne
                                                       diacylglycerol acyltransferase;
                                                                                     Ryegrass diacylglycerol acyltransferase, DGAT,
                                                                                                                  10-FEB-2005
                                                                                                                                                ADU81175;
                                                                                                                                                                           ADU81175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetically engineering the biosynthetic pathways in plants involved in
the accumulation of sterol compounds and tocopherol to produce compounds
for lowering the level of low density lipoprotein cholesterol in blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venkatramesh M, Corbin
Kishore GM, Lardizabal
                                          fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match:
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                                                                                                                                                                                                                                                                                                                                                                        434 MetMetAlaGlnIleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsnTyrGly
                                                                                                                                                                                                                                                                 474
                                                                                                                                                                                                                                                                                                               454 AshAlaAlaValTrpLeuSerLeuIleIleGlyGlnProIleAlaValLeuMetTyrVal
                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                        w
                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                        HisAspTyrTyrValLeuAsnTyrGluAlaPro 484
                                                                                                                                                                                                                                                                                              AATGCAGCTGTGTGGGTGACACTCATCATTGGGCAACCGGTGGCTGT-CTCATGTATGTC
                                                                                                                                                                                                                                                                                                                                                       ATGATGGCTCAGGTCCCACTGGCCTGGATTGTGGGCCGATTCTTCCAAGGGAACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 62-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US009696
                                                                                                                  (first entry)
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232.00
96.1%
86.3%
8.9%
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Lassner MW,
                                                        DGAT; plant breeding; crop improvement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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W, Rangwala SH,
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U;
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Karunanandaa
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 RESULT 13
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a new substantially purified or isolated nucleic acid or its fragment from a ryegrass (Lolium) or fescue (Festuca) species encodes a diacylglycerol acyltransferase 1 (DGATI) or DGATI-like polypeptide or its fragment or variant. The nucleic acid or nucleic acid fragment and/or its nucleotide sequence information or single nucleotide polymorphism of perennial ryegrass Lolium perenne is useful as a molecular genetic marker or for modifying fatty acid biosynthesis in a plant. The present sequence represents a plant diacylglycerol acyltransferase, DGAT, cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like polypeptide, useful as a genetic marker or for modifying fatty acid biosynthesis in a plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 400 BP; 91 A; 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 38; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-821891/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bryan GT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2003; 2003AU-00902413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-2004; 2004WO-AU000635
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360
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                                                                                                                                                                         181
                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                            413
                                                                                                                                                                                                                                                                                                                     393
                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGRIC VICTORIA SERVICES AGRESEARCH LTD.
                                                                                                                                                                                                                               GTGCTCCATGAGTTATGTGTTGCTGTCCCCTGCCGAATTGTCAAGTTCTGGCATTCTTA
                                                                                                                                                                                                                                                                                                           MetLeuArgArgGlySerSerLysTrpMetAlaArgThrGlyValPheLeuAlaSerAla
                                                                                                                                                                                                                                                                                                                                                PheTrpGlnAsnTrpAsnIleProValHisLysTrpCysIleArgHisPheTyrLysPro
                      MetTyrValHisAspTyrTyrValLeuAsn 480
                                                                                                               GATACAATGGCCGGCAACATGATATTCTGGTTCTTTTTTCTGCATCTACGGACAGCCTATG
                                                                                                                                                                                             GlyMetMetAlaGlnIleProLeu------AlaTrpPheValGlyArgPhePhe
                                                                                                                                                                                                                                                       PhePheHisGluTyrLeuValSerValProLeuArgMetPheArgLeuTrpAlaPheThr
CTGTACTACCATGAT----GTGATGAAT 383
                                                       CCGGCAACATGATATTCTGGTTCTTTTCTGC-ATCTACGGACAGCCTATGTGCGTTCTC
                                                                                                                                           GlnGlyAsnTyrGlyAsnAlaAlaValTrp-----
                                                                                                                                                                         GGGATCATGCTGCAGATCCCTCTTATCATATTGACATCATACCTGAAGAGCAAATTCAGA 240
                                                                                                                                                                                                                                                                                       CCCAGGCGCAGTGGTATATCAAAGGAAGTTGCTGTCTTTGTATCATTTTTTGTATCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burling MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                   1.05e-11
222.50
50.8%
39.2%
8.6%
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                                                                                    ---LeuSerLeuileIleGlyGlnProIleAlaValLeu 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G; 131 T; 0
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Mismatches:
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432

412

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120

448

458

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ACH92522/c

ID ACH92522;

XX

ACH92522;

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29-JUI-2004 (first entry)

XX

DE

Human genome derived single exity

XX

Human, probe; ss; gene express

KW

Human, probe; ss; gene express

CO

SA

ME

16-CCT-2003.

XX

US2003194704-A1.

XX

VS2003194704-A1.

XX

VS2003194704-A1.

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PD

16-CCT-2003.

XX

(PENN/) PENN S G.
PA

(RANK/) RANK D R.
PA

(PT

PO

(COT-2003.

COT PT

PO

RANK D R.
PA

(RANK/) RANK
                                                                                                                                                                                                                                                                       Constiguous amino acids of any of the 27,400 fully defined nucleic expression, comprising any of the 27,400 fully defined nucleotide encoding at least 8 amino acids of any of the 6888 amino acid sequences of fully defined in the specification. The probe is a single exon probe that complements or tragments, and construction acid sequences of fully defined in the specification. The probe is a single exon probe that comprising a plurality of single exon probe that compressed in human cells or tissues. Also included are a spatially-compressed in human cells or tissues. Also included are a spatially-compressed in human comprising a plurality of single exon nucleic acid gene expression (comprising a plurality of single exon nucleic acid gene expression (comprising a plurality of single exon nucleic acid gene expression, a vector comprising the single exon probe cited above, where each of the plurality of plurality), a single contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of acustomer desiring to measure gene expression, a method of providing contends of selling and/or licensing single exon probes or microarrays to contend acids and apparatus are useful in gene corrected actors and acids and apparatus are useful in gene corrected actors and the probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross alternatives splicing events, in priming the synthesis of nucleic acids.
                                             seqdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                       or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                      smaller genomic alterations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 25717; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2002; 2002US-00029386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; probe; ss; gene expression; single exon alternative splicing event; genomic alteration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid probe for measuring human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human genome-derived single exon nucleic acid probes useful for human e expression analysis, for identifying or characterizing alternative icing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-00029386.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression; single exon probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK;
                                                                                                                                                                                                                                                      in priming the synthesis of nucleic acids
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RESULT 14
AAD40442
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 121
                                                                                                                                                                                                                                                                    primer_bind
                                                                                                                                                                                                                                                                                                                                                                                               Bovine diacylglycerol acyltransferase (DGAT1) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD40442
Determining genetic merit of a bovine with respect and volume for improved milk production, comprises
                          WPI; 2002-500128/53
                                                                                                                                             06-DEC-2000;
                                                                                                                                                    31-OCT-2000;
                                                                                                                                                                       31-OCT-2001;
                                                                                                                                                                                        10-MAY-2002.
                                                                                                                                                                                                         WO200236824-A1
                                                                                                                                                                                                                                           primer_bind
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                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                      DGAT1; polymorphism;
                                                                                                                                                                                                                                                                                                                                                                              Bovine; diacylglycerol acyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-2002
                                                                                                        (COPP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No . :
                                                                                                                          (GEOR/)
                                                                      SPEL/
                                                                                       (REID/)
                                                                                                 SNEL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                          MAJ, Coppieters, Spelman RJ;
                                                                             SNELL R G.
REID S J.
FORD C A.
                                                                      SPELMAN R J.
                                                                                                        GRISART B M J.
                                                                                                                           GEORGES M A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlnProIleAlaValLeuMetTyrValHisAspTyrTyrValLeuAsnTyrGluAlaPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyArgPhePheGlnGlyAsnTyrGlyAsnAlaAlaValTrpLeuSerLeuIleIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCCAATAGCCGTCCTCATGTACGTCCACGACTACTACGTGCTCAACTATGAGGCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCGCTTTTTCCAGGGCAACTATGGCAACGCAGCTGTGTGGCTGTCGCTCATCATCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP;
                                                                                                                                            2000NZ-00507888
2000NZ-00508662
                                                                                                                                                                       2001WO-NZ000245
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                            /*tag= c
/bound_moiety= '
379. .400
                                                                                                                                                                                                                                                                                               /bound_moiety= "DGAT123"
complement(225. .244)
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers complement (27. .46)
                                                                                                                                                                                                                                                                     /bound_moiety= "DGAT1 21"
243. .264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 A; 30 C;
                                                                                                                                                                                                                        /bound_moiety= "DGAT1 22"
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                                                     Grisart
                                                                                                                                                                                                                                                     "DGAT1 24B"
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Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 U; 0 Other;
                                                     BMJ,
                                                                                                                                                                                                                                                                                                                                                                       transgenic;
                                                                                                                                                                                                                                                                                                                                                                               genotyping;
                                                     Snell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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0
                                                                                                                                                                                                                                                                                                                                                                        enzyme;
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to milk composition determining the
                                                                                                                                                                                                                                                                                                                                                                               milk production;
                                                                                                                                                                                                                                                                                                                                                                                                 Q allele
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ARESULT 15
ARZ45387
ID ARZ45
XX ARZ45
AC ARZ45
XX ARZ45
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Acyl-CoA:cholesterol acyltransferase; ACAT; ACAT-like protein; sterol;
                                                   Acyl-CoA: cholesterol acyltransferase (ACAT)-like protein partial DNA.
                                                                                                                      27-MAR-2000
                                                                                                                                                                                                                                   AAZ45387 standard;
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                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a partial sequence of a polynucleotide CC encoding an acyl-CoA:cholesterol acyltransferase (ACAT) related protein. CC The ACAT-like protein is active in the formation of a sterol, ester CC and/or triacylglycerol from a fatty acyl-CoA and sterol and/or CC diacylglycerol substrate. The DNA can be used for modifying the lipid CC composition of plant cells. The ACAT-like protein has diacylglycerol cc acyltransferase (DAGAT) activity, and so the synthesis of triglycerides CC can be suppressed or increased using the DNA. The protein can be used to CC produce plant oils with a modified triglyceride content. The products can CC also be used to identify antagonists and agonists of DAGAT activity. Such CC ameliorating diseases associated with DAGAT activity, including cancer, diabetes, tardiopulmonary diseases e.g. heart CC associated with altered cellular diacylglycerol concentration or PKC astivity, including cancer, diabetes, tardiopulmonary diseases e.g. heart CC fibroblatoma, metabolic disorders, obesity, diseases associated with CC abnormal lipid metabolism, and diseases associated with abnormal fat CC absorption, lipoprotein secretion and adipogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel polynucleotides used for modifying plant oil composition and for developing products for treating e.g. cancer, diabetes, cardiopulmonary disease or metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ester; triacylglycerol; fatty acyl-CoA; lipid composition; plant cell; diacylglycerol acyltransferase; DAGAT; triglyceride; cancer; diabetes; cardiopulmonary disease; heart failure; atherosclerosis; adipocytosis; leukaemia; skin carcinoma; fibroblastoma; metabolic disorder; obesity; abnormal lipid metabolism; abnormal fat absorption;
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12-NOV-1998;
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GGATGGACAAATTTCCGTGGATTCTTCAATTTGTCTATTTTACTTTTGGTACTTTCAAAT
                                                                                                           SerGlyHisTrpGluLeuArgCysHisArgLeuGlnAspSerLeuPheSerSerAspSer
                                                                          AGAGGACCTTGCGAGAAAGTGGTACATACTGCTCAAGATTCAT
                                                                                                                                                  CCAGTAGACGCTCCTCATTTGCACAAAATGGTAATTCGTCAAGGGAAAAGTTCAGAAATG
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN-0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=500
-MOST=abss01h -USER=US10659800 @CGN 1 14939 @runat 05052006 122306 17192
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-NCPU=6 -TCPU=3 -NO_MMAp -NEG SCORES=0 -XGAFOD=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAP6P=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Kgapop 10.0 , Ygapext
Kgapop 6.0 , Fgapext
belop 6.0 , Delext
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Sequence 4664 from Patent WO0192581.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Sequence 5894 from Pater
CQ463116
CQ463116.1 GI:41428735
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                                                                                                                                                                                                                                                                                                                                                                                                                      MetGlnPheGlyAspArgGluPheTyrArgAspTrpTrpAsnSerGluSerValThrTyr
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CORPORATION (US)
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US-10-659-800-6 (1-488) x CQ463116 (1-371)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 201)

Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M.,

Cantor, C.R. and Braun, A.

Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
                                                                                                                                                                                                                                                                                       Sequenom, Inc.
3595 John Hopkins Court, San
Tel: 18582029018
Fax: 18582029020
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                                                                                                                                                                                                                      Email: abraun@sequenom.com
primer A: No primer sequence
Primer B: No primer sequence
STS size: 201.
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                                                                                                                                                                                                                                                                                                                                                                             Contact: Andreas Braun
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                                                                                                 /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/clone lib="Human DNA (Se
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3.41e-19
367.00
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Length:
Matches:
Conservative:
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BV207926
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Best Local Similarity:
Query Match:
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Tel: 18582029018
Fax: 18582029020
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Primer B: No primer sequence
STS size: 201.
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Large-Scale Validation of Single Nucleotide Polymorphisms in
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sqnm224934 Human
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1 (bases 1 to 201)
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/clone lib="Human DNA (Se
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HisAspTyrTyrValLeuAsnTyrGluAlaPro
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434 MetMetAlaGlnIleProLeuAlaTrpPheValGlyArgPhePheGlnGlyAsnTyrGly
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CALGENE LLC
OS Mus 8p. (murine)
OS Mus 8p. (murine)
PN JP 2002517201-A/12
PD 18-JUN-1999 JP 2000552290
PF 04-JUN-1999 UP 2000552290
PR 05-JUN-1998 US 60/088143,12-NOV-1998 US 60/108389 PI
MICHAEL W LASSNER, DIANE M RUEZINSKY
PC C12N15/09,A01H5/00,C11B1/00,C11C3/00,C12N1/21,C12N5/10,C12N9/PC 10,C12N15/00,
PC C12N5/00
CC Acyl CoA:cholesterol acyltransferase related nucleic acid CC
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1 (bases 1 to 299)
Lassner, M.W. and Ruezinsky, D.M.
Acyl CoA:cholesterol acyltransferase re-
Acyl CoA:cholesterol acyltransferase re-
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JP 2002517201-A/12.
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                                          AATGCAGCTGTGTGGGTGACACTCATCATTGGGCAACCGGTGGCTGT-CTCATGTATGTC
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Location/Qualifiers
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/mol_type="genomic DNA'
/db_xref="taxon:10095"
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DEFINITION
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AR227750
AR227750.1
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                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                 Plant sterol acyltransferases
Patent: WO 0116308-A 31 08-MAR-2001;
MONSANTO COMPANY (US)
                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                      Sequence 31 from Patent AX090338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 299)
Lassner, M.W. and Ruezinsky, D.M.
Acyl CoA: cholesterol acyltransferase
                                                                                                                                   Lassner, M. and van Eenennaam, A.
                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                           AX090338.1 GI:13444204
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LLC; Davis, CA;
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/mol_type="genomic |
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                                                               organism="Mus musculus"
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US-10-659-800-6 (1-488) x BD241860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 OS Caenorhabditis elegans (nematode)
PN JP 2002517201-A/17
PD 118-JUN-2002
PF 04-JUN-1999 JP 2000552290
PR 05-JUN-1998 US 60/088143,12-NOV-1998 US 60/108389 PI
MICHAEL W LASSNER, DIANE M RUEZIMSKY
PC C12N15/09, A01H5/00, C11B1/00, C11C3/00, C12N1/21, C12N5/10, C12N9/PC 10, C12N15/00,
PC C12N15/00,
PC C12N5/00
CC n at position 46 is unknowd
FH Key

Location/Qdalifiers
FT misc_feature (46).
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Lassner,M.W. and Ruezinsky,D.M.
Acyl CoA:cholesterol acyltransf@rase related
Patent: JP 2002517201-A 17 18-JUN-2002;
CALGENE LLC
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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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JP 2002517201-A/17
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AGAGGACCTTGCGAGAAAGTGGTACATACTGCTCAAGATTCATTGTTTTCGACGAGTTCT
                     SerGlyHisTrpGluLeuArgCysHisArgLeuGlnAspSerLeuPheSerSerAspSer 80
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                                                                                                              ProAlaProAlaProAsn---
                                                                                                                                                                                                                                                                                                                                                        /organism="Caenorhabditis
/mol_type="genomic DNA*
/db_xref="taxon:6239"
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AR227755
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Sequence
AR227755
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Lassher, M.W. and Ruezinsky, D.M.
Acyl CoA: cholesterol acyltransferase
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/mol_type="genomic
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AR422734
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PN JP 2002010789-A/10364

PD 15-JAN-2002

PF 07-AUG-2000 JP 2000280989

PR 05-AUG-2000 JP 2000280989

PR 05-AUG-1999 US 60/147499

PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVI GIORDANO

PC C12N15/09, C12N15/09, C07K14/47, C07K16/1

PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00

CC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00

CC C12N15/00

CC EST and encoded human protein FH Key Location/Qualifiers FT source 1. 113

FT Source 1. 113
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AR422734
       1 (bases 1 to 113)
Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 14231 28-OCT-2003;
                                                                                    Unknown
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Edwards, J.B.D.M., Jobert, S. and Giordano, J.
EST and encoded human protein
Patent: JP 2002010789-A 10364 15-JAN-2002;
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 Genset S.A.;;
                                                                                                     Unknown
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EST and encoded human protein.
                                                                      Unclassified
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Mammalia; Eutheria; Euarchontoglires; Primates; Cata
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05-AUG-1999 US 60/147499
JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN
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Acyl CoA:cholesterol acyltransferase related nucleic acid sequences. BD241847
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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AR227742
1 (bases 1 to 275)
Lassner, M.W. and Ruezinsky, D.M.
Acyl CoA: cholesterol acyltransferase
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JP 2002517201-A/4.
Glycine max (soybean)
                                           Unknown
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OS GLYVINE max (soybean)

PN JP 2002517201-A/4

PD 18-JUN-2002

PF 04-JUN-1999 JP 2000552290

PF 04-JUN-1998 US 60/088143,12-NOV-1998 US 60/

MICHAEL W LASSNER, DIANE M RUEZINSKY

PC C12N15/00, A01H5/00,C11B1/00,C11C3/00,C12N1/21,C12

PC C12N15/00,

PC C12N5/00,

PC C12N5/00,

CC n at positions 192, 202, 204, 211, 222, 234, 238,

CC 262, and 263 is unknown

FH Key

Location/Qualifiers

FT misc_feature (192)...(263).
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Acyl CoA: cholesterol acyltransferase related
Patent: JP 2002517201-A 4 18-JUN-2002;
CALGENE LLC
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Glycine max
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
cosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Sequence 45 from Patent
AX090352
AX090352.1 GI:13444213
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Patent: US 6444876-)
Calgene LLC; Davis,
WOX;
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Patent: WO 0116308-A 45 08-MAR-2001;
MONSANTO COMPANY (US)
                                                                                                                                                                                                                                                                                                                        Glycine max (soybean)
Glycine max
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LLC; Davis, CA;
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P	DRUG RESPONSE, METHODS OF	Sequence 188102 Sequence 801511 Sequence 44, Ap Sequence 1352, equence 18673, Sequence 150111 Sequence 763520 Sequence 6062, Sequence 3737,	quence 159095, equence 252023, equence 490003, quence 152023, equence 252023, equence 552470, quence 555470, equence 555470, equence 510628, equence 510628, equence 51306, equence 51306, equence 51306, equence 51306, equence 51306, equence 51306, equence 51307, equence 5137506, quence 137508, quence 137508, quence 137508, quence 137508, quence 137508, equence 137508, quence 1375	Description Sequence 13119, A Sequence 13111, A Sequence 64752, A Sequence 64751, A Sequence 64750, A Sequence 64750, A Sequence 47, Appl Sequence 47, Appl

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GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS AGSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METI

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLO01559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FRANTSCH GOT WINDOWS Version 4.0

SEQ ID NO 13118

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens
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Sequence 13111, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
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Sequence 64752, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS TITLE OF INVENTION: DETECTION AND USES THER FILE OF INVENTION: DETECTION AND USES THER FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64752
LENGTH: 201
                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo:
US-10-995-561-64752
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US-10-995-561-64752
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                                                                   US-10-659-800-6 (1-488)
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TITLE OF INVENTION: DETECTION AND USES TO
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13111
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                         ArgAspTrpTrpAsnSerGluSerValThrTyrPheTrpGlnAsnTrpAsnIleProVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheTyrArgAspTrpTrpAsnSerGluSerValThrTyrPheTrpGlnAsnTrpAsnIle 379
CAGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACGTGGTG
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GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RE:
DETECTION AND USES THEREOF
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
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Alignment Scores:
Pred. No.:
Score:
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CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ, ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 64750

LENGTH - 201
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US-10-995-561-64711
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                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-64750
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Best Local Similarity:
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; ORGANISM: Homo sapiens
US-10-995-561-64711
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ. ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                    Sequence 64750; Application US/10995561 Publication No. US20050272054A1
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Publication No. US20050272054A1
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 GENERAL INFORMATION:
                Sequence 12018, Application US/11096568A Publication No. US20060048240A1
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SEQ ID NO 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kim, MyungSoon
APPLICANT: Woo, SukKyung
TITLE OF INVENTION: METHOD FOR DETECTING METHYLATION OF PROMOTER USING
TITLE OF INVENTION: ENZYME AND DNA CHIP
FILE REFERENCE: 4240-113
CURRENT APPLICATION NUMBER: US/10/983,809
CURRENT FILING DATE: 2004-11-08
PRIOR APPLICATION NUMBER: KR 10-2004-0075395
PRIOR PILING DATE: 2004-09-21
NUMBER OF SEQ ID NOS: 48
COLUMN OF SEQ ID NOS: 48
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ORGANISM: Homo
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                                                                                                    GTGTGCGGAGTAGGGGTGGGTGGGGGAATTGGAAG
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                                                                                                                                                                            GlyGlyGlyProAlaAlaAlaGluGluGluValArgAspAlaAlaAlaGlyProAspVal
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Oh, TaeJeong
Yoon, DaeKyoung
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Query Match:
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; OTHER INFORMATION: Ceres Seq.
US-11-096-568A-12018
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            PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILLING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILLING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILLING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILLING DATE: 2001-05-09
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TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 12018
LENGTH: 462
TYPE - 1218
LENGTH: 462
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                                                                                                                                                                                                                                                                                                                                            Sequence 159095, Application US/09925065A Publication No. US20040181048A1
                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping
TITLE OF INVENTION: Nucleotide Polymorphisms i.
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Triticum aestivum FEATURE: NAME/KEY: misc feature
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; ORGANISM: Homo sapiens
US-09-925-065A-159095
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                                                             US-10-659-800-6 (1-488) x US-10-301-480-252022
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Query Match:
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publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
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SEQ ID NO 159095
LENGTH: 444
                                                                                                                                                                                                                                                                              SEQ ID NO 252022
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/301,480 CURRENT FILING DATE: 2002-11-21 PRIOR APPLICATION NUMBER: US 10/215,598 PRIOR FILING DATE: 2002-08-09 PRIOR APPLICATION NUMBER: US 60/311,695
                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows
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TYPE: DNA
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ArgArgArgArgThrGlySerArgProSer----SerHisGlyGlyGlyGlyPro---
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 865431
LENGTH: 452
RESULT 12
US-09-925-065A-490003
; Sequence 490003, Application US/09925065A
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US-10-301-480-865431
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Best Local Similarity:
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US-10-301-480-865431
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US-09-925-065A-159096
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US-09-925-065A-490003
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
CONTENTED: Each of the Middle Nosion of the Middle 
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                                Sequence 159096, Application US/0925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human
FILE REFERENCE: 108827.135
TITLE OF INVENTION: Nucleotide FILE REFERENCE: 108827.135
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Matches:
Conservative:
Mismatches:
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Sequence 252023, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wand, David G.
TITLE OF INVENTION: Identifiction and Mapping of TITLE OF INVENTION: In the Human Genome FILE REFERENCE; 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FASTSEQ for Windows Version 4.0
1 SEQ ID NO 252023
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-252023
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US-10-301-480-252023
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DB:
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-159096
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 159096
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Indels:
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Sequence 865432, Application US/10301480
Publication No. US20060057564A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identifiction and Mapping of TITLE OF INVENTION: It the Human Genome FILE REFERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2002-08-09
PRIOR PRICATION NUMBER: US 10/311,695
PRIOR APPLICATION NUMBER: US 0/311,695
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SEQ ID NO 865432
LENGTH: 452
TYPE: DNA
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NUMBER OF SEQ ID NOS: 1226818
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AlaGlyAspAlaProAlaProAlaProAsnLysAspGlyAspAlaGlyValGlySerGly
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                                                                          -----AlaAlaAlaGluGluGluValArgAspAlaAlaAlaGlyProAspValGlyAla 42
                                                                                                           ArgArgArgArgThrGlySerArgProSer----SerHisGlyGlyGlyGlyPro---
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Matches:
Conservative:
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Indels:
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Minimum
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*
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Gapop 10.0 , Gapext 0.5
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US-10-207-817-544
US-10-307-817-544
US-10-659-800-6
US-11-117-005-5
US-10-741-600-1339
US-10-741-600-1341
US-10-1415-620-5
US-10-4415-620-5
US-10-4415-620-5
US-10-4415-620-5
US-10-4415-620-5
US-10-415-620-5
US-10-415-620-7
US-10-273-438-7
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US-10-659-800-10
US-10-659-800-10
US-10-659-800-10
US-10-415-620-65
US-10-73-438-5
US-10-731-438-5
US-10-731-438-5
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US-10-659-800-5
US-10-659-800-5
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US-10-273-438-6
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Result No.

ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cases, Robert V.

APPLICANT: Cases, Sylvaine

APPLICANT: Erickson, Sandra

TITLE OF INVENTION: Diacyldycerol O-Acyltransferase

FILE REFERENCE: UCAL-105CIPS

CURRENT APPLICATION NUMBER: US/10/273,438

CURRENT APPLICATION NUMBER: US/10/40,315

PRIOR APPLICATION NUMBER: US/10/040,315

PRIOR FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: US/10/771

PRIOR FILING DATE: 1998-11-09

PRIOR APPLICATION NUMBER: US/10/883

PRIOR APPLICATION NUMBER: 09/103,754

PRIOR FILING DATE: 1998-06-23

NUMBER OF SEQ ID NOS: 10

COUTABLE SEG ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LENGTH: 488
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-273-438-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 2594; DB 4; Best Local Similarity 100.0%; Pred. No. 8.9e-233; Matches 488; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10273438 Publication No. US20030072757A1
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                                                                                                                                                                                                                                                                                         61 SGHWELRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDPIQV 120
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APPLICANT: Earese, Robert V.
APPLICANT: Cases, Sylvaine
APPLICANT: Smith, Steven
APPLICANT: Erickson, Sandra
TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
FILE REFERENCE: UCAL-105CIP2
CURRENT APPLICATION NUMBER: US/10/040,315A
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/107,771
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/US98/17883
PRIOR APPLICATION NUMBER: PCT/US98/17883
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1999-06-23
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US-10-040-315A-6
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Best Local S
Matches 488
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US-10-307-817-544

Sequence 544, Application US/10307817

Publication No. US20040058338A1

GENERAL INFORMATION:

APPLICANT: Agee et al.

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE: 21402-502C
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-307-817-544
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CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 544
LENGTH: 488
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                                                                                                             YRDWWNSESVTYFWQNWNIFVHKWCIRHFYKFMLRRGSSKWWARTGVFLASAFFHEYLVS 420
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APPLICANT: Cases, Sylvaine
APPLICANT: Cases, Sylvaine
APPLICANT: Smith, Steven
APPLICANT: Smith, Steven
ITILE OF INVENTION: Diacylglycerol O-Acyltransferase
FILE REFERENCE: UCAL-105CIP2CON2
CURRENT APPLICATION NUMBER: US/10/659,800
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 10/040,315
PRIOR APPLICATION NUMBER: 60/107,771
PRIOR APPLICATION NUMBER: 60/107,771
PRIOR APPLICATION NUMBER: PCT/US99/17883
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 10
SOPTWARE: FastSEQ for Windows Version 3.0
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US-10-659-800-6
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TYPE: PRT
ORGANISM: homo sapiens
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                                                       VPLRMFRLMAPTGMMAQIFLAWFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLN
                                                                                                                              YRDWWNSESVTYFWQNWNIFVHKWCIRHFYKFMLRRGSSKWMARTGVFLASAFFHEYLVS
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YEAPAAEA
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; LENGTH: 488
; TYPE: PRT
; ORGANISM: human
US-11-117-005-5
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FILE REFERENCE: 3015-5684.IUS
CURRENT APPLICATION NUMBER: US/11/117,005
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: PCT/CA99/01202
PRIOR APPLICATION NUMBER: BCT/CA99/01202
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 26
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US-11-117-005-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 2594; DB 6; Best Local Similarity 100.0%; Pred. No. 8.9e-233; Matches 488; Conservative 0; Mismatches 0;
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APPLICANT: Taylor, David C
APPLICANT: Wei, Yangdou
APPLICANT: Jako, Colette C
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                                 YEAPAAEA 488
                                                                                          VPLRMFRLWAFTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLN
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                                                                     VPLRMFRLWAFTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAVLMYVHDYYVLN
                                                                                                                                          YRDWWNSESVTYFWQNWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFLASAFFHEYLVS
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YEAPAAEA 488
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RESULT

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Sequence 1341, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECT
FILE REFERENCE: CLO01499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FASTSEQ for Windows Version 4.0
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US-10-741-600-1341
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1339
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Publication No. US20050026169A1

GENERAL INFORMATION: Michele et al.
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, MYCCARDIAL INFARCTION, METHODS OF DETECTION INTILE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION INFILE REFERENCES: CL001499

FILE REFERENCES: CL001499

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT APPLICATION NUMBER: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1339
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Pred. No. 3.2e-232;
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Sequence 17, Application US/10157855

| Sequence 17, Application US/10091A1 |
| GENERAL INFORMATION:
| APPLICANT: Lassner, Michael W. |
| APPLICANT: Ruezinsky, Diane M. |
| TITLE OF INVENTION: Acid Sequences |
| FILE REFERENCE: 16516.158 |
| CURRENT APPLICATION NUMBER: US/10/157,855 |
| CURRENT APPLICATION NUMBER: 09/326,203 |
| PRIOR FILING DATE: 1998-06-05 |
| PRIOR APPLICATION NUMBER: 09/326,203 |
| PRIOR APPLICATION NUMBER: 00/088,143 |
| PRIOR FILING DATE: 1998-06-05 |
| PRIOR FILING DATE: 1998-105-05 |
| PRIOR FILING DATE: 1998-06-05 |
| PRIOR FILING DATE: 1998-11-12 |
| NUMBER: 05 EDETATION NUMBER: 07 10 |
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1341
US-10-157-855-17
                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 17
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Best Local Similarity
                    TYPE: PRT ORGANISM: Rattus
                                                                           LENGTH:
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Pred. No. 3.2e-232;
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88.6%;

Score 2299.5;

DB 4;

Length

180 169

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Sequence 24, Application US/10647517

| Sequence 24, Application US/20050102716A1
| GENERAL INFORMATION: US20050102716A1
| GENERAL INFORMATION: COMPANY
| TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF INTITLE OF INVENTION: COMPOUNDS AND TOCOPHEROLS
| FILE REFERENCE: MTC 6462.1
| CURRENT APPLICATION NUMBER: US/10/647,517
| CURRENT FILING DATE: 2003-08-26
| PRIOR APPLICATION NUMBER: US/09/548,256
| PRIOR APPLICATION NUMBER: US/09/548,256
| PRIOR APPLICATION NUMBER: 60/128,995
| PRIOR FILING DATE: 1999-04-12
| PRIOR FILING DATE: 1999-04-12
| NUMBER OF SEQ ID NOS: 31
| COPETMANDE: DESCRIPTIONS: 31
                                                                                                                                                                              ; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 500
; TYPE: PRT
; ORGANISM: rat
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Best Local Similarity
Matches 427; Conserv
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                                                 MGDRGGAGSSRRRTGSRVSIQGGSGPMVDEEEVRDAAVGPDLGAGGDAPAPAPVPAPAH
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                                                                                                                Score 2299.5; DB 5;
Pred. No. 2.7e-205;
Pred. Mismatches 31;
                                                                                                                 Indels
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SEQ ID NO 2
LENGTH: 489
TYPE: PRT
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/415,620 CURRENT FILING DATE: 2003-04-29 NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: REID, SUZANNE J
APPLICANT: FORD, CHRISTINE A
APPLICANT: GEORGES, MICHEL A J
APPLICANT: COPPIETERS, MOUTER H
APPLICANT: GRISART, BERNARD M J
APPLICANT: SNELL, RUSSELL G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SPELMAN, RICHARD J
TITLE OF INVENTION: MARKER ASSISTED SELECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: P452508 CJE
                                                             NAME/KEY: misc_feature
LOCATION: (10402)..(10417)
OTHER INFORMATION: ambiguous
                                                                                                                NAME/KEY: misc feature
LOCATION: (9496)..(9496)
OTHER INFORMATION: ambign
FEATURE:
                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (9434)..(9434)
OTHER INFORMATION: ambig
                                                                                                                                                                                                                                                           PEATURE: FEATURE: NAME/KP: misc_feature LOCATION: (8315)...(8317) OTHER INFORMATION: translation
                                                                                                                                                                                                                                                                                                                             ORGANISM: Bos taurus
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   Score 2292.5; DB 4
Pred. No. 1.2e-204;
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                    Length 489;
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467

420

480

407 360 347

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Sequence 5, Application US/10415620
Publication No. US20040076977A1
GENERAL INFORMATION:
APPLICANT: REID, SUZANNE J
APPLICANT: FORD, CHRISTINE A
APPLICANT: FORD, CHRISTINE A
APPLICANT: GENGES, MICHEL A J
APPLICANT: GENGES, MICHEL A J
APPLICANT: GRISART, BERNARD M J
APPLICANT: SNELL, RUSSELL G
APPLICANT: SNELL, RUSSELL G
APPLICANT: SPELMAN, RICHARD J
TITLE OF INVENTION: MARKER ASSISTED SELECTION OF
FILE REFERENCE: P452508 CJE
CURRENT APPLICATION NUMBER: US/10/415,620
CURRENT FILING DATE: 2003-04-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.1
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US-10-415-620-5
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                                                         US-10-415-620-5
Query Match
Best Local S
Matches 434
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                                                                 LENGTH: 489

TYPE: PRT
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: VARIANT
LOCATION: (232)..(232)
OTHER INFORMATION: ases 7224-7225 of the genomic sequence (measured from the adening OTHER INFORMATION: residue of the translation start codon). Lysine (K) corresponds
OTHER INFORMATION: to the Q allele, alanine (A) corresponds to the q allele.
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Score 2292.5; DB 4;
Pred. No. 1.2e-204;
5; Mismatches 31;
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; TYPE: PRT
; ORGANISM: Bos t
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                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10482936

Publication No. US20040234986A1

GENERAL IMPORMATION:

APPLICANT: Arbeitsgemeinschaft Deutscher Rinderzochter e.V.

TITLE OF INVENTION: Method of testing a mammal for its predisposition for TITLE OF INVENTION: marbling

FILE REFERENCE: F 1078 EP

CURRENT APPLICATION NUMBER: US/10/482,936

CURRENT FILING DATE: 204-04-05

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 433; Conser
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 IQVVSLFLKDPHSWPAPCLVIAANVFAVAAFQVEKRLAVGALTEQAGLLLHVANLATILC
                                                                                                                                     MGDR---GSSRRRRTGSRPSSHGGGGPAAAEEEVRDAAAGPDVGAAGDAPAPAPNKDGDA
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                                                           DVGSGHWNLRCHRLQDSLFSSDSGFSNYRGILNWCVVMLILSNARLFLENLIKYGILVDP
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                                                                                                                     MGDRGGAGGSRRRRTGSRPSIQGGSGPAAAEEEVR-----DVGAGGDAPVRDTDKDGDV
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                                                                                                                                                                             Score 2278.5; DB 5;
Pred. No. 2.3e-203;
Pred. No. 3.3;
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APPLICANT: ZOU, Jitao
APPLICANT: Tâylor, David C
APPLICANT: Wei, Yangdou
APPLICANT: Wei, Yangdou
APPLICANT: Jako, Colette C
TITLE OF INVENTION: Diacylglycerol Acyl Transferase Gene from Plants
FILE REFERENCE: 3015-564.1US
CURRENT APPLICATION UNMBER: US/11/117,005
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR APPLICATION NUMBER: 09/623,514
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 26
SED THARE: Patentin Ver. 2.1
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; TYPE: PRT
; ORGANISM: mouse
US-11-117-005-4
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Publication No. US20050193446A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                       Matches 421;
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LATIICFPAAVALLVESITPVGSVFALASYSIMFLKLYSYRDVNLWCRQRRVKAKAVSTG
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GENERAL INFORMATION:

APPLICANT: Farese, Robert V.

APPLICANT: Cases, Sylvaine

APPLICANT: Cases, Sylvaine

APPLICANT: Erickson, Sandra

ITILE OF INVENTION: Diacyldycerol O-Acyltransferase

FILE REFERENCE: UCAL-105CIP2

CURRENT APPLICATION NUMBER: US/10/273,438

CURRENT APPLICATION NUMBER: US/10/040,315

PRIOR APPLICATION NUMBER: E0/107,771

PRIOR FILING DATE: 2001-10-29

PRIOR FILING DATE: 1998-11-09

PRIOR APPLICATION NUMBER: ECT/US98/17883

PRIOR APPLICATION NUMBER: DCT/US98/17883

PRIOR APPLICATION NUMBER: 09/339,472

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1998-06-23

NUMBER OF SEG ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 498
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; TYPE: PRT
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Best Local Similarity
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                                                                                                      GILVDPIQVVSLFLKDPYSWPAPCVIIASNIFVVAAFQIEKRLAVGALTEQMGLLLHVVN
                                                    LATILCEPAAVVLLVESITEVGSLLALMAHTILFLKLFSYRDVNSWC--RRARAKAASAG
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KKASSAAAPHTVSYPDNLTYRDLYYFLFAPTLCYELNFPRSPRIRKRFLLRRILEMLFFT
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                                 LATIICFPAAVALLVESITPVGSVFALASYSIMFLKLYSYRDVNLWCRQRRVKAKAVSTG
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84.8%; Pred. No.: 7e-203;
tive 29; Mismatches 3
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CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US/10/040,315
PRIOR FILING DATE: 2001-10-29
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/US98/17883
PRIOR APPLICATION NUMBER: PCT/US98/17883
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR APPLICATION NUMBER: 09/103,754
PRIOR APPLICATION NUMBER: 09/339,472
PRIOR APPLICATION NUMBER: 09/339,472
PRIOR FILING DATE: 1998-06-23
NUMBER OF SEQ ID NOS: 10
SCOTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 498
TYPE: PRT
ORGANISM: mud I
JS-10-273-438-10
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Best Local S
Matches 420
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APPLICANT: Cases, Sylvaine
APPLICANT: Smith, Steven
APPLICANT: Exickson, Sandra
TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
FILE REFERENCE: UCAL-105CIP2
FILE REFERENCE: UCAL-105CIP2
                                         181
                                                          172 LATILCFPAAVVLLVESITFVGSLLALMAHTILFLKLFSYRDVNSWC--RRARAKAASAG
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Similarity 84.8%; Pred. No. 7e-203;
20; Conservative 29; Mismatches 3
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                                                                                                                                    TSAFFHEYLVSVPLRMFRLWAFTAMMAQVPLAWIVGRFFQGNYGNAAVWVTLIIGQPVAV
                                                                                          AELLOFGDREFYRDWWNAESVTYFWONWNI PVHKWCIRHFYKPMLRHGSSKWVARTGVFL
                                                        ASAFFHEYLVSVPLRMFRLWAFTGMMAQIPLAWFVGRFFQGNYGNAAVWLSLIIGQPIAV 469
                                                                                                      AELMOFGDREFYRDWWNSESVTYFWONWNIPVHKWCIRHFYKPMLRRGSSKWMARTGVFL 409
 LMYVHDYYVLNYDAP
                                                                                            420
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